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Attorney Docket No. 15966-697 (Cura-197)

COMBINED DECLARATION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am an original, first and sole inventor of the subject matter (an original, first and joint inventor) which is claimed and for which a utility patent is sought on the invention entitled:

NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING THE SAME

the specification of which is attached hereto.

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56.

I hereby claim the benefit under Title 35, United States Code, § 119(e) or §120 of any United States application(s), or §365(c) of any PCT International application(s) designating the United States of America listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

Application No. *(U.S.S.N.)*	**Filing Date** *(dd/mm/yy)*	**Status** *(Patented, Pending, Abandoned)*
60/186,592	03/03/00	Pending
60/186,718	03/03/00	Pending
60/190,400	17/03/00	Pending
60/187,294	06/03/00	Pending
60/196,018	07/04/00	Pending
60/259,548	03/01/00	Pending
60/187,293	06/03/00	Pending

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or patent issued thereon.

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NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

RELATED APPLICATIONS

This application claims priority from USSN 60/186,592, filed March 3, 2000; USSN 60/186,718, filed March 3, 2000; USSN 60/187,293, filed March 6, 2000; USSN 60/187,294, filed March 6, 2000; USSN 60/190,400, filed March 17, 2000; ; USSN 60/196,018, filed April 7, 2000; USSN 60/259,548, filed January 3, 2001; each of which is incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

The invention relates generally to polynucleotides and polypeptides, as well as vectors, host cells, antibodies, and recombinant methods for producing these nucleic acids and polypeptides.

SUMMARY OF THE INVENTION

The invention is based in part upon the discovery of novel nucleic acid sequences encoding novel polypeptides. The disclosed FCTR1, FCTR2, FCTR3, FCTR4, FCTR5, FCTR6 and FCTR7 nucleic acids and polypeptides encoded therefrom, as well as derivatives, homologs, analogs and fragments thereof, will hereinafter be collectively designated as "FCTRX" nucleic acid or polypeptide sequences.

In one aspect, the invention provides an isolated FCTRX nucleic acid molecule encoding a FCTRX polypeptide that includes a nucleic acid sequence that has identity to the nucleic acids disclosed in SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24. In some embodiments, the FCTRX nucleic acid molecule will hybridize under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule that includes a protein-coding sequence of a FCTRX nucleic acid sequence. The invention also includes an isolated nucleic acid that encodes a FCTRX polypeptide, or a fragment, homolog, analog or derivative thereof. For example, the nucleic acid can encode a polypeptide at least 80% identical to a polypeptide comprising the amino acid sequences of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25. The nucleic acid can be, for example, a genomic DNA fragment or a cDNA molecule that

includes the nucleic acid sequence of any of SEQ ID NOS: 1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24.

Also included in the invention is an oligonucleotide, *e.g.*, an oligonucleotide which includes at least 6 contiguous nucleotides of a FCTRX nucleic acid (*e.g.*, SEQ ID NOS: 1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24) or a complement of said oligonucleotide.

Also included in the invention are substantially purified FCTRX polypeptides (SEQ ID NO: 2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25). In certain embodiments, the FCTRX polypeptides include an amino acid sequence that is substantially identical to the amino acid sequence of a human FCTRX polypeptide.

The invention also features antibodies that immunoselectively-binds to FCTRX polypeptides, or fragments, homologs, analogs or derivatives thereof.

In another aspect, the invention includes pharmaceutical compositions that include therapeutically- or prophylactically-effective amounts of a therapeutic and a pharmaceutically-acceptable carrier. The therapeutic can be, *e.g.*, a FCTRX nucleic acid, a FCTRX polypeptide, or an antibody specific for a FCTRX polypeptide. In a further aspect, the invention includes, in one or more containers, a therapeutically- or prophylactically-effective amount of this pharmaceutical composition.

In a further aspect, the invention includes a method of producing a polypeptide by culturing a cell that includes a FCTRX nucleic acid, under conditions allowing for expression of the FCTRX polypeptide encoded by the DNA. If desired, the FCTRX polypeptide can then be recovered.

In another aspect, the invention includes a method of detecting the presence of a FCTRX polypeptide in a sample. In the method, a sample is contacted with a compound that selectively binds to the polypeptide under conditions allowing for formation of a complex between the polypeptide and the compound. The complex is detected, if present, thereby identifying the FCTRX polypeptide within the sample.

The invention also includes methods to identify specific cell or tissue types based on their expression of a FCTRX.

Also included in the invention is a method of detecting the presence of a FCTRX nucleic acid molecule in a sample by contacting the sample with a FCTRX nucleic acid probe or primer, and detecting whether the nucleic acid probe or primer bound to a FCTRX nucleic acid molecule in the sample.

In a further aspect, the invention provides a method for modulating the activity of a FCTRX polypeptide by contacting a cell sample that includes the FCTRX polypeptide with a

compound that binds to the FCTRX polypeptide in an amount sufficient to modulate the activity of said polypeptide. The compound can be, *e.g.*, a small molecule, such as a nucleic acid, peptide, polypeptide, peptidomimetic, carbohydrate, lipid or other organic (carbon containing) or inorganic molecule, as further described herein.

Also within the scope of the invention is the use of a Therapeutic in the manufacture of a medicament for treating or preventing disorders or syndromes including, *e.g.*, Colorectal cancer, adenomatous polyposis coli, myelogenous leukemia, congenital ceonatal alloimmune thrombocytopenia, multiple human solid malignancies, malignant ovarian tumours particularly at the interface between epithelia and stroma, malignant brain tumors, mammary tumors, human gliomas, astrocytomas, mixed glioma/astrocytomas, renal cells carcinoma, breast adenocarcinoma, ovarian cancer, melanomas, renal cell carcinoma , clear cell and granular cell carcinomas, autocrine/paracrine stimulation of tumor cell proliferation, autocrine/paracrine stimulation of tumor cell survival and tumor cell resistance to cytotoxic therapy, paranechmal and basement membrane invasion and motility of tumor cells thereby contributing to metastasis, tumor-mediated immunosuppression of T-cell mediated immune effector cells and pathways resulting in tumor escape from immune surveilance, neurological disorders, neurodegenerative disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie-Tooth neuropathy, demyelinating Gardner syndrome, familial myelodysplastic syndrome; mental health conditions, immunological disorders, allergy and infection, asthma, bronchial asthma, Avellino type eosinophilia, lung diseases, reproductive disorders, male infertility, female reproductive system disorders, male and female reproductive diseases, hemangioma, deafness, glycoprotein Ia deficiency, desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases like diabetes, Schistosoma mansoni infection, Spinocerebellar ataxia, Plasmodium falciparum parasitemia, Corneal dystrophy - Groenouw type I, Corneal dystrophy - lattice type I, and Reis-Bucklers corneal dystrophy. The Therapeutic can be, *e.g.*, a FCTRX nucleic acid, a FCTRX polypeptide, or a FCTRX-specific antibody, or biologically-active derivatives or fragments thereof.

The invention further includes a method for screening for a modulator of disorders or syndromes including, *e.g.*, Also within the scope of the invention is the use of a Therapeutic in the manufacture of a medicament for treating or preventing disorders or syndromes including, *e.g.*, Colorectal cancer, adenomatous polyposis coli, myelogenous leukemia, congenital ceonatal alloimmune thrombocytopenia, multiple human solid malignancies, malignant ovarian tumours particularly at the interface between epithelia and stroma, malignant brain tumors, mammary tumors, human gliomas, astrocytomas, mixed glioma/astrocytomas, renal cells carcinoma, breast

adenocarcinoma, ovarian cancer, melanomas, renal cell carcinoma , clear cell and granular cell carcinomas, autocrine/paracrine stimulation of tumor cell proliferation, autocrine/paracrine stimulation of tumor cell survival and tumor cell resistance to cytotoxic therapy, paranechmal and basement membrane invasion and motility of tumor cells thereby contributing to metastasis, tumor-mediated immunosuppression of T-cell mediated immune effector cells and pathways resulting in tumor escape from immune surveilance, neurological disorders, neurodegenerative disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie-Tooth neuropathy, demyelinating Gardner syndrome, familial myelodysplastic syndrome; mental health conditions, immunological disorders, allergy and infection, asthma, bronchial asthma, Avellino type eosinophilia, lung diseases, reproductive disorders, male infertility, female reproductive system disorders, male and female reproductive diseases, hemangioma, deafness, glycoprotein Ia deficiency, desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases like diabetes, Schistosoma mansoni infection, Spinocerebellar ataxia, Plasmodium falciparum parasitemia, Corneal dystrophy - Groenouw type I, Corneal dystrophy - lattice type I, and Reis-Bucklers corneal dystrophy. The method includes contacting a test compound with a FCTRX polypeptide and determining if the test compound binds to said FCTRX polypeptide. Binding of the test compound to the FCTRX polypeptide indicates the test compound is a modulator of activity, or of latency or predisposition to the aforementioned disorders or syndromes.

Also within the scope of the invention is a method for screening for a modulator of activity, or of latency or predisposition to an disorders or syndromes including, *e.g.*, Also within the scope of the invention is the use of a Therapeutic in the manufacture of a medicament for treating or preventing disorders or syndromes including, *e.g.*, Colorectal cancer, adenomatous polyposis coli, myelogenous leukemia, congenital ceonatal alloimmune thrombocytopenia, multiple human solid malignancies, malignant ovarian tumours particularly at the interface between epithelia and stroma, malignant brain tumors, mammary tumors, human gliomas, astrocytomas, mixed glioma/astrocytomas, renal cells carcinoma, breast adenocarcinoma, ovarian cancer, melanomas, renal cell carcinoma , clear cell and granular cell carcinomas, autocrine/paracrine stimulation of tumor cell proliferation, autocrine/paracrine stimulation of tumor cell survival and tumor cell resistance to cytotoxic therapy, paranechmal and basement membrane invasion and motility of tumor cells thereby contributing to metastasis, tumor-mediated immunosuppression of T-cell mediated immune effector cells and pathways resulting in tumor escape from immune surveilance, neurological disorders, neurodegenerative disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie-Tooth neuropathy,

demyelinating Gardner syndrome, familial myelodysplastic syndrome; mental health conditions, immunological disorders, allergy and infection, asthma, bronchial asthma, Avellino type eosinophilia, lung diseases, reproductive disorders, male infertility, female reproductive system disorders, male and female reproductive diseases, hemangioma, deafness, glycoprotein Ia deficiency, desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases like diabetes, Schistosoma mansoni infection, Spinocerebellar ataxia, Plasmodium falciparum parasitemia, Corneal dystrophy - Groenouw type I, Corneal dystrophy - lattice type I, and Reis-Bucklers corneal dystrophy by administering a test compound to a test animal at increased risk for the aforementioned disorders or syndromes. The test animal expresses a recombinant polypeptide encoded by a FCTRX nucleic acid. Expression or activity of FCTRX polypeptide is then measured in the test animal, as is expression or activity of the protein in a control animal which recombinantly-expresses FCTRX polypeptide and is not at increased risk for the disorder or syndrome. Next, the expression of FCTRX polypeptide in both the test animal and the control animal is compared. A change in the activity of FCTRX polypeptide in the test animal relative to the control animal indicates the test compound is a modulator of latency of the disorder or syndrome.

In yet another aspect, the invention includes a method for determining the presence of or predisposition to a disease associated with altered levels of a FCTRX polypeptide, a FCTRX nucleic acid, or both, in a subject (*e.g.*, a human subject). The method includes measuring the amount of the FCTRX polypeptide in a test sample from the subject and comparing the amount of the polypeptide in the test sample to the amount of the FCTRX polypeptide present in a control sample. An alteration in the level of the FCTRX polypeptide in the test sample as compared to the control sample indicates the presence of or predisposition to a disease in the subject. Preferably, the predisposition includes, *e.g.*, Also within the scope of the invention is the use of a Therapeutic in the manufacture of a medicament for treating or preventing disorders or syndromes including, *e.g.*, Colorectal cancer, adenomatous polyposis coli, myelogenous leukemia, congenital ceonatal alloimmune thrombocytopenia, multiple human solid malignancies, malignant ovarian tumours particularly at the interface between epithelia and stroma, malignant brain tumors, mammary tumors, human gliomas, astrocytomas, mixed glioma/astrocytomas, renal cells carcinoma, breast adenocarcinoma, ovarian cancer, melanomas, renal cell carcinoma , clear cell and granular cell carcinomas, autocrine/paracrine stimulation of tumor cell proliferation, autocrine/paracrine stimulation of tumor cell survival and tumor cell resistance to cytotoxic therapy, paranechmal and basement membrane invasion and motility of tumor cells thereby contributing to metastasis, tumor-mediated immunosuppression of T-cell

mediated immune effector cells and pathways resulting in tumor escape from immune surveilance, neurological disorders, neurodegenerative disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie-Tooth neuropathy, demyelinating Gardner syndrome, familial myelodysplastic syndrome; mental health conditions, immunological disorders, allergy and infection, asthma, bronchial asthma, Avellino type eosinophilia, lung diseases, reproductive disorders, male infertility, female reproductive system disorders, male and female reproductive diseases, hemangioma, deafness, glycoprotein Ia deficiency, desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases like diabetes, Schistosoma mansoni infection, Spinocerebellar ataxia, Plasmodium falciparum parasitemia, Corneal dystrophy - Groenouw type I, Corneal dystrophy - lattice type I, and Reis-Bucklers corneal dystrophy. Also, the expression levels of the new polypeptides of the invention can be used in a method to screen for various cancers as well as to determine the stage of cancers.

In a further aspect, the invention includes a method of treating or preventing a pathological condition associated with a disorder in a mammal by administering to the subject a FCTRX polypeptide, a FCTRX nucleic acid, or a FCTRX-specific antibody to a subject (*e.g.*, a human subject), in an amount sufficient to alleviate or prevent the pathological condition. In preferred embodiments, the disorder, includes, *e.g.*, Also within the scope of the invention is the use of a Therapeutic in the manufacture of a medicament for treating or preventing disorders or syndromes including, *e.g.*, Colorectal cancer, adenomatous polyposis coli, myelogenous leukemia, congenital ceonatal alloimmune thrombocytopenia, multiple human solid malignancies, malignant ovarian tumours particularly at the interface between epithelia and stroma, malignant brain tumors, mammary tumors, human gliomas, astrocytomas, mixed glioma/astrocytomas, renal cells carcinoma, breast adenocarcinoma, ovarian cancer, melanomas, renal cell carcinoma , clear cell and granular cell carcinomas, autocrine/paracrine stimulation of tumor cell proliferation, autocrine/paracrine stimulation of tumor cell survival and tumor cell resistance to cytotoxic therapy, paranechmal and basement membrane invasion and motility of tumor cells thereby contributing to metastasis, tumor-mediated immunosuppression of T-cell mediated immune effector cells and pathways resulting in tumor escape from immune surveilance, neurological disorders, neurodegenerative disorders, nerve trauma, familial myelodysplastic syndrome, Charcot-Marie-Tooth neuropathy, demyelinating Gardner syndrome, familial myelodysplastic syndrome; mental health conditions, immunological disorders, allergy and infection, asthma, bronchial asthma, Avellino type eosinophilia, lung diseases, reproductive disorders, male infertility, female reproductive system disorders, male and female reproductive diseases, hemangioma, deafness, glycoprotein Ia deficiency, desmoid disease, turcot syndrome,

liver cirrhosis, hepatitis C, gastric disorders, pancreatic diseases like diabetes, Schistosoma mansoni infection, Spinocerebellar ataxia, Plasmodium falciparum parasitemia, Corneal dystrophy - Groenouw type I, Corneal dystrophy - lattice type I, and Reis-Bucklers corneal dystrophy.

In yet another aspect, the invention can be used in a method to identity the cellular receptors and downstream effectors of the invention by any one of a number of techniques commonly employed in the art. These include but are not limited to the two-hybrid system, affinity purification, co-precipitation with antibodies or other specific-interacting molecules.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION

The invention is based, in part, upon the discovery of novel nucleic acid sequences that encode novel polypeptides. The novel nucleic acids and their encoded polypeptides are referred to individually as FCTR1, FCTR2, FCTR3, FCTR4, FCTR5, FCTR6, and FCTR7. The nucleic acids, and their encoded polypeptides, are collectively designated herein as “FCTRX”.

The novel FCTRX nucleic acids of the invention include the nucleic acids whose sequences are provided in Tables 1A, 2A, 3A, 3C, 3E, 3F, 3G, 3H, 4A, 5A, 5C, 5E, 6A, 6C, and 7A inclusive (“Tables 1A - 7A”), or a fragment, derivative, analog or homolog thereof. The novel FCTRX proteins of the invention include the protein fragments whose sequences are provided in Tables 1B, 2B, 3B, 3I, 4B, 5B, 5D, 6B, 6D, and 7B inclusive (“Tables 1B - 7B”). The individual FCTRX nucleic acids and proteins are described below. Within the scope of this invention is a method of using these nucleic acids and peptides in the treatment or prevention of a disorder related to cell signaling or metabolic pathway modulation.

FCTR1

Novel FCTR1 is a growth factor ("FCTR") protein related to follistatin-like gene, and mac25. FCTR1 (also referred to by proprietary accession number 58092213.0.36) is a full-length clone of 771 nucleotides, including the entire coding sequence of a 105 amino acid protein from nucleotides 438 to 753. The clone was originally obtained from thyroid gland, kidney, fetal kidney, and spleen tissues.

The nucleotide sequence of FCTR1 as presently determined is reported in Table 1A. The start and stop codons are bolded and the 5' and 3' untranslated regions are underlined.

Table 1A. FCTR1 nucleotide sequence (SEQ ID NO:1).

GGTCCTCACCCCCTTCCTCTCTCCCAGCCTCGGTGTCTGGTTACGGCTCCTCTGCTCGCATTGTGACTTTGGCCAGGCTGGGGGA
AATGACCCGGGAGGGTCCCATGCGGCTACATAAAATTGGCAGCCTTAGAACTAGTGGGAAGGCGGGTGCGCGAAGTCGAGGGGCGG
AGAGAGGGGGCCGGAGGAGCTGCTTTCTGAATCCAAGTTCGTGGGCTCTCTCAGAAGTCCTCAGGACGGAGCAGAGGTGGCCGGCG
GGCCCGGCTGACTGCGCCTCTGCTTTCTTTCCATAACCTTTTCTTTCGGACTCGAATCACGGCTGCTGCGAAGGGTCTAGTTCCGG
ACACTAGGGCCCCAGATCGTGTCACATCCATATGACACTTGGAATGTGACAGGGCAGGATGTGATCTTTGGCTGTGAAGTGTTTGC
CTACCCC**ATG**GCCTCCATCGAGTGGAGGAAGGATGGCTTGGACATCCAGCTGCCAGGGGATGACCCCCACATCTCTGTGCAGTTTA
GGGGTGGACCCCAGAGGTTTGAGGTGACTGGCTGGCTGCAGATCCAGGCTGTGCGTCCCAGTGATGAGGGCACTTACCGCTGCCTT
GCCCGCAATGCCCTGGGTCAAGTGGAGGCCCCTGCTAGCTTGACAGTGCTCACACCTGACCAGCTGAACTCTACAGGCATCCCCCA
GCTGCGATCACTAAACCTGGTTCCTGAGGAGGAGGCTGAGAGTGAAGAGAATGACGATTACTAC**TAG**GTCCAGAGCTCTGGCC

The predicted amino acid sequence of FCTR1 protein corresponding to the foregoing nucleotide sequence is reported in Table 1B. FCTR1 was searched against other databases using SignalPep and PSort search protocols. The protein is most likely located in the cytoplasm (certainty=0.6500) and seems to have no N-terminal signal sequence. The predicted molecular weight of FCTR1 protein is 11711.8 daltons.

Table 1B. Encoded FCTR1 protein sequence (SEQ ID NO:2).

MASIEWRKDGLDIQLPGDDPHISVQFRGGPQRFEVTGWLQIQAVRPSDEGTYRCLARNALGQVEAPASLTVLTPDQLNSTGIPQLR
SLNLVPEEEAESEENDDYY

FCTR1 was initially identified with a TblastN analysis of a proprietary sequence file for a follistatin-like probe or homolog which was run against the Genomic Daily Files made available by GenBank. A proprietary software program (GenScan™) was used to further predict the nucleic acid sequence and the selection of exons. The resulting sequences were further modified by means of similarities using BLAST searches. The sequences were then manually corrected for apparent inconsistencies, thereby obtaining the sequences encoding the full-length protein.

In an analysis of sequence databases, it was found, for example, that the FCTR1 nucleic acid sequence has 31/71 bases (43%) identical and 46/71 bases positively alike to a *Mus Musculus* IGFBP-like protein (TREMBL Accession Number:BAA21725) shown in Table 1C. In all BLAST alignments herein, the "E-value" or "Expect" value is a numeric indication of the probability that the aligned sequences could have achieved their similarity to the BLAST query

sequence by chance alone, within the database that was searched. For example, as shown in Table 1C, the probability that the subject ("Sbjct") retrieved from the FCTR1 BLAST analysis, in this case the *Mus Musculus* IGFBP-like protein, matched the Query FCTR1 sequence purely by chance is $1.2x10^{-11}$.

Table 1C. BLASTP of FCTR1 against *Mus Musculus* IGFBP-like protein (SEQ ID NO:38)

```
PTNR:REMTREMBL-ACC:BAA21725 IGFBP-LIKE PROTEIN - MUS MUSCULUS (MOUSE), 270 AA.
LENGTH = 270

 SCORE = 161 (56.7 BITS), EXPECT = 1.2E-11, P = 1.2E-11
 IDENTITIES = 31/71 (43%), POSITIVES = 46/71 (64%)

QUERY:     9 DGLDIQLPGDDPHISVQFRGGPQRFEVTGWLQIQAVRPSDEGTYRCLARNALGQVEAPAS 68
             +||+ +||||  +|+||  ||||    | | |+ |   +|   ||| | | | ||+|+ ++  +
SBJCT:   191 EGLE-ELPGDHVNIAVQVRGGPSDHETTSWILINPLRKEDEGVYHCHAANAIGEAQSHGT 249

QUERY:    69 LTVLTPDQLNS 79
             +|||  ++  |
SBJCT:   250 VTVLDLNRYKS 260
```

The amino acid sequence of FCTR1 also had 26/58 bases (44%) identical, and 38/58 bases (65%) positive for *Mus Musculus* Follistatin-like Protein shown in Table 1D.

Table 1D. BLASTP of FCTR1 against *Mus Musculus* Follistatin-like Protein (SEQ ID NO:39)

```
PTNR:SPTREMBL-ACC:Q61581 FOLLISTATIN-LIKE 2 (FOLLISTATIN-LIKE PROTEIN) - MUS MUSCULUS
(MOUSE), 238 AA.
            LENGTH = 238

 SCORE = 149 (52.5 BITS), EXPECT = 1.5E-10, P = 1.5E-10
 IDENTITIES = 26/58 (44%), POSITIVES = 38/58 (65%)

QUERY:    15 LPGDDPHISVQFRGGPQRFEVTGWLQIQAVRPSDEGTYRCLARNALGQVEAPASLTVL 72
             ||||   ++++| ||||++ |||||+ +   +    | | | | | |+ ||   | | +||+
SBJCT:   165 LPGDRENLAIQTRGGPEKHEVTGWVLVSPLSKEDAGEYECHASNSQGQASAAAKITVV 222
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The amino acid sequence of FCTR1 also had 26/58 bases (44%) identical, and 38/58 bases (65%) positive for *Homo sapiens* MAC25 protein shown in Table 1E.

Table 1E. BLASTP of FCTR1 against *Homo sapiens* MAC25 protein (SEQ ID NO:40)

```
PTNR:SPTREMBL-ACC:Q07822 MAC25 PROTEIN - HOMO SAPIENS (HUMAN), 277 AA.
            LENGTH = 277

 SCORE = 149 (52.5 BITS), EXPECT = 3.2E-10, P = 3.2E-10
 IDENTITIES = 26/58 (44%), POSITIVES = 38/58 (65%)

QUERY:    15 LPGDDPHISVQFRGGPQRFEVTGWLQIQAVRPSDEGTYRCLARNALGQVEAPASLTVL 72
             ||||   ++++| ||||++ |||||+ +   +    | | | | | |+ ||   | | +||+
SBJCT:   209 LPGDRDNLAIQTRGGPEKHEVTGWVLVSPLSKEDAGEYECHASNSQGQASASAKITVV 266
```

The amino acid sequence of FCTR1 also had 26/58 bases (44%) identical, and 38/58 bases (65%) positive for *Mus musculus* MAC25 protein shown in Table 1F.

Table 1F. BLASTP of FCTR1 against *Mus musculus* MAC25 protein (SEQ ID NO:41)

```
PTNR:SPTREMBL-ACC:O88812 MAC25 - MUS MUSCULUS (MOUSE), 281 AA
            LENGTH = 281

 SCORE = 149 (52.5 BITS), EXPECT = 3.4E-10, P = 3.4E-10
 IDENTITIES = 26/58 (44%), POSITIVES = 38/58 (65%)

QUERY:     15 LPGDDPHISVQFRGGPQRFEVTGWLQIQAVRPSDEGTYRCLARNALGQVEAPASLTVL 72
              ||||  ++++| ||||++ |||||+ +  +   | | | | |+|  ||  | | |+||+
SBJCT:    208 LPGDRENLAIQTRGGPEKHEVTGWVLVSPLSKEDAGEYECHASNSQGQASAAAKITVV 265
```

The amino acid sequence of FCTR1 also had 26/58 bases (44%) identical, and 38/58 bases (65%) positive for *Homo sapiens* Prostacyclin-stimulating factor shown in Table 1G.

Table 1G. BLASTP of FCTR1 against *Homo sapiens* Prostacyclin-stimulating factor (SEQ ID NO:42)

```
PTNR:SPTREMBL-ACC:Q16270 PROSTACYCLIN-STIMULATING FACTOR - HOMO SAPIENS (HUMAN), 282
AA
            LENGTH = 282

 SCORE = 149 (52.5 BITS), EXPECT = 3.4E-10, P = 3.4E-10
 IDENTITIES = 26/58 (44%), POSITIVES = 38/58 (65%)

QUERY:     15 LPGDDPHISVQFRGGPQRFEVTGWLQIQAVRPSDEGTYRCLARNALGQVEAPASLTVL 72
              ||||  ++++| ||||++ |||||+ +  +   | | | | |+|  ||  | | |+||+
SBJCT:    209 LPGDRDNLAIQTRGGPEKHEVTGWVLVSPLSKEDAGEYECHASNSQGQASASAKITVV 266
```

The amino acid sequence of FCTR1 also had 18/44 bases (40%) identical, and 25/44 bases (56%) positive for rat Colorectal cancer suppressor shown in Table 1H.

Table 1H. BLASTP of FCTR1 against rat Colorectal cancer suppressor (SEQ ID NO:43)

```
PTNR:PIR-ID:B40098 COLORECTAL CANCER SUPPRESSOR DCC - RAT (FRAGMENTS)
            LENGTH = 144

 SCORE = 78 (27.5 BITS), EXPECT = 1.1E-05, SUM P(2) = 1.1E-05
 IDENTITIES = 18/44 (40%), POSITIVES = 25/44 (56%)

QUERY:     33 FEVTGW--LQIQAVRPSDEGTYRCLARNALGQVEAPASLTVLTP 74
              |++ |   |+|  |  |||| |+|+| |  |  ++ | | |  |
SBJCT:    101 FQIVGGSNLRILGVVKSDEGFYQCVAENEAGNAQSSAQLIVPKP 144

 SCORE = 37 (13.0 BITS), EXPECT = 1.1E-05, SUM P(2) = 1.1E-05
 IDENTITIES = 8/19 (42%), POSITIVES = 12/19 (63%)

QUERY:      1 MASIEWRKDGLDIQL-PGD 18
              | +| |+|+   |+   |||
SBJCT:     30 MPTIHWQKNQQDLTPNPGD 48
```

The amino acid sequence of FCTR1 also had 32/83 bases (38%) identical, and 45/83 bases (54%) positive to bases 55-137, and 24/68 bases (35%) identical, and 37/68 bases (54%) positive to bases 166-225 of *Homo sapiens* PTPsigma-(Brain) Precursor shown in Table 1I.

Table 1I. BLASTP of FCTR1 against *Homo sapiens* PTPsigma-(Brain) Precursor (SEQ ID NO:44)

```
PTNR:TREMBLNEW-ACC:AAD09360 PTPSIGMA-(BRAIN) PRECURSOR - HOMO SAPIENS (HUMAN), 1502
AA.
            LENGTH = 1502

 SCORE = 109 (38.4 BITS), EXPECT = 0.00010, P = 0.00010
 IDENTITIES = 32/83 (38%), POSITIVES = 45/83 (54%)

QUERY:     14 QLPGDD-PHISVQFRG---GPQRFEVTGW-------LQIQAVR-PSDEGTYRCLARNALG 61
              |  ||   | ++   +|     ||||    +       |+|| +| | ||   | |+|+|++|
SBJCT:     55 QATGDPKPRVTWNKKGKKVNSQRFETIEFDESAGAVLRIQPLRTPRDENVYECVAQNSVG 114

QUERY:     62 QVEAPASLTVLTPDQLNSTGIPQL 85
              ++   | ||||  ||| | | | +
SBJCT:    115 EITVHAKLTVLREDQLPS-GFPNI 137

 SCORE = 77 (27.1 BITS), EXPECT = 0.25, P = 0.22
 IDENTITIES = 24/68 (35%), POSITIVES = 37/68 (54%)

QUERY:      4 IEWRKDGLDIQLPGDDPHISVQFRGGPQRFEVTGWLQIQAVRPSDEGTYRCLARNALG-Q 62
              | | || | +      ||  |      |  ++    +| |||++    +|+| | |+|  |+ | +
SBJCT:    166 ITWFKDFLPV-----DPSAS---NGRIKQLR-SGALQIESSEETDQGKYECVATNSAGVR 216

QUERY:     63 VEAPASLTV 71
                +||+| |
SBJCT:    217 YSSPANLYV 225
```

The amino acid sequence of FCTR1 also had 32/83 bases (38%) identical, and 45/83 bases (54%) positive for amino acids 55-137 and 26/69 bases (37%) identical, and 38/69 (54%) positive for amino acids 166-234 of *Homo sapiens* Protein-Tyrosine Phosphatase Sigma shown in Table 1J.

Table 1J. BLASTP of FCTR1 against *Homo sapiens* PTPsigma-(Brain) Precursor (SEQ ID NO:45)

```
PTNR:SPTREMBL-ACC:Q13332 PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, S PRECURSOR (EC
3.1.3.48) (PROTEIN-TYROSINE PHOSPHATASE SIGMA) (R-PTP-SIGMA) (PTPRS) - HOMO SAPIENS
(HUMAN), 1948 AA.
LENGTH = 1948

 SCORE = 109 (38.4 BITS), EXPECT = 0.00013, P = 0.00013
 IDENTITIES = 32/83 (38%), POSITIVES = 45/83 (54%)

QUERY:     14 QLPGDD-PHISVQFRG---GPQRFEVTGW-------LQIQAVR-PSDEGTYRCLARNALG 61
              |  ||   | ++   +|     ||||    +       |+|| +| | ||   | |+|+|++|
SBJCT:     55 QATGDPKPRVTWNKKGKKVNSQRFETIEFDESAGAVLRIQPLRTPRDENVYECVAQNSVG 114

QUERY:     62 QVEAPASLTVLTPDQLNSTGIPQL 85
              ++   | ||||  ||| | | | +
SBJCT:    115 EITVHAKLTVLREDQLPS-GFPNI 137

 SCORE = 88 (31.0 BITS), EXPECT = 0.023, P = 0.022
 IDENTITIES = 26/69 (37%), POSITIVES = 38/69 (55%)
```

```
QUERY:     4 IEWRKDGLDIQLPGDDPHISVQFRGGPQRFEVT---GWLQIQAVRPSDEGTYRCLARNAL 60
             | | || |  +      +  |   | |    + || |    | |||++    +|+| | |+| |+
SBJCT:   166 ITWFKDFLPVDPSASNGRIK-QLRS--ETFESTPIRGALQIESSEETDQGKYECVATNSA 222

QUERY:    61 G-QVEAPASLTV 71
             | +   +||+| |
SBJCT:   223 GVRYSSPANLYV 234
```

A ClustalW analysis comparing the protein of the invention with related protein sequences is given in Table 1K, with FCTR1 shown on line 2. In the ClustalW alignment of the FCTR1 protein, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be mutated to a much broader extent without altering protein structure or function.

Table 1K. ClustalW Analysis of FCTR1

```
1)     Q07822 MAC25 PROTEIN.(SEQ ID NO:40)
2)     Q16270 PROSTACYCLIN-STIMULATING FACTOR.(SEQ ID NO:42)
       3)Q61581_FOLLISTATIN-LIKE 2: FOLLISTATIN-LIKE 2 (FOLLISTATIN-LIKE PROTEIN) (SEQ
            ID NO:39)
4)     BAA21725 IGFBP-LIKE PROTEIN (SEQ ID NO:38)
5)     FCTR1 (SEQ ID NO:2)
6)     B40098 COLORECTAL CANCER SUPPRESSOR DCC - RAT (FRAGMENTS) (SEQ ID NO:43)

Q07822      MERASLRALLFGPAGLLLLLLPLSSSSSSDTCGPCEPASCPPLPPLGCLLGETRDACGCC
Q16270      MERPSLRALLLGAAGLLLLLLPLSSSSSSDTCGPCEPASCPPLPPLGCLLGETRDACGCC
Q61581_     MERP PRALLLGAAGLLLLLLPLSSSSSSDACGR
BAA21725    MPRLPLLLLLLLPSLARGLGLRDAG  RRHPECSPCQQDRCPAPSPCPAPWISARDECGCC
FCTR1
B40098

Q07822      PMCARGEGEPCGGGAGRGYCAPGMECVKSRKRRRGKAGAAAGGPGVSGVCVCKSRVPVC
Q16270      PMCARGEGEPCGGGAGRGYCAPGMECVKSRKRRKGKAGAAAGGPGVSGVCVCKSRYPVC
Q61581_                      RGHCAPGMECVKSRKRRRGKAGAAAGGPATLAVCVCKSRYPVC
BAA21725    ARCLGAEGASCG  GPVGSRCGPGLVCA SR     ASGTAPEG  T GLCVCAQRGAVC
FCTR1
B40098                                                        PLRFLSQTESIT

Q07822      GSDGTTYPSGCQLRAASQRAESRGEKA   ITQVSKGTCEQGPSIVTPPKDIWNVTGAQV
Q16270      GSDGTTYPSGCQLRAASQRAESRGEKA   ITQVSKGTCEQGPSIVTPPKDIWNVTGAQV
Q61581_     GSNGITYPSGCQLRAASLRAESRGEKP   ITQVSKGTCEQGPSIVTPPKDIWNVTGAKV
BAA21725    GSDGRSYSSICALRLRARHAPRAHHGH   LHKARDGPCEFAPVVLMPPRDIHNVTGTQV
FCTR1
B40098      AFMGDTVLLKCEVIGDPMPTIHWQKNQQDLTPNPGDSRVVVPPWFLNHPSNLYAYESMDI

Q07822      YLSCEVIGIPTPVLIWNKVKRGHYGVQRTELLPGDRDNLAIQTRGGPEKHEVTGWVLVSP
Q16270      YLSCEVIGIPTPVLIWNKVKRGHYGVQRTELLPGDRDNLAIQTRGGPEKHEVTGWVLVSP
Q61581_     FLSCEVIGIPTPVLIWNKVKRDHSGVQRTELLPGDRENLAIQTRGGPEKHEVTGWVLVSP
BAA21725    ELSCEVKAVPTPVITWKKVKHSPEGTEGLEELPGDHVNIAVQVRGGPSDHETTSWILINP
FCTR1             MASIEWRKDGLDIO.......LPGDDPHISVQFRGGPQRFEVTGWLQIQA
B40098      EFECAVSGKPVPTVNWMKNGDVVV............ISDYFQIVGGSN.......LRILG

Q07822      LSKEDAGEYECHASNSQGQASASAKITVVDALHEIAS................EKR....
Q16270      LSKEDAGEYECHASNSQGQASASAKITVVDALHEIPV................KKGEGAE
Q61581_     LSKEDAGEYECHASNSQGQASAAAKITVVDALHEIPL................KKGEGAQ
BAA21725    LRKEDEGVYHCHAANAIGEAQSHGTVTVLDLNRYKSL................YSSVPGD
FCTR1       VRPSDEGTYRCLARNALGQVEAPASLTVLTPDQLNSTGIPQLRSLNLVPEEEAESEENDD
B40098      VVKSDEGFYQCVAENEAGNAQSSAQLIVPKP.............................
```

```
Q07822
Q16270      L.
Q61581_     L.
BAA21725    LL
FCTR1       YY
```

IGFBP is expressed in neurostem cell and developing central nervous system. MAC-25, a follistatin like protein is a growth suppressor of osteosarcoma cells, and meningiomas. DCC is expressed in most normal tissues especially in colonic mucosa, but is deleted in colorectal cancers.

Since FCTR1 has similarity to these proteins (shown in BlastP, Tables 1C-1J, and in clustalW, Table 1K) it is likely that it has similar function. Therefore FCTR1 could function as on or more of the following: a tumor suppressor geneor regulator of neurological system development.

Based on the protein similarity and tissue expression, FCTR1 may be useful in the following diseases and uses:

(i) Tissue regeneration in vitro and in vivo

(ii) Neurological disorders, neurodegenerative disorders, nerve trauma

(iii) Reproductive health

(iv) Immunological disorders, allergy and infection

(v) In cancer as a diagnostic and prognostic marker, as well as a protein therapeutic

FCTR2

FCTR2 (alternatively referred to herein as AC012614_1.0.123), is a growth factor bearing sequence similarity to human KIAA1061 protein and to genes involved in neuronal development and reproductive physiology (e.g., cell adhesion molecules, follistatin, roundabout and frazzled). FCTR2 is a full-length clone of 5502 nucleotides, including the entire coding sequence of a 815 amino acid protein. This sequence is expressed in glioma, osteoblast, other cancer cells, lung carcinoma, small intestine (This sequence maps to Unigene Hs.123420 which is expressed in brain, breast, kidney, pancreas, pooled tissue).

A FCTR2 ORF begins with an ATG initiation codon at nucleotides 420-422 and ends with a TGA codon at nucleotides 2865-2867. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 2A, and the start and stop codons are in bold letters.

Table 2A. FCTR2 Nucleotide Sequence (SEQ ID NO:3).

```
CAATTTCACACAGGAAACAGCTATGCCATGATTACGCAAGTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTG
TGCTGGAATTCGGCTTACTCACTATAGGGCTCGAGCGGCTGCCCGGGCAGGTCATTAATTCCATTTCTTTTTAGAGTATC
ACAGCTTTCTCCTTCACTGACCACCCTTTGCTTCCTGTCAGAAAGCCCTGGACAGAACTCTCTGTGGGATTCTGCCCATG
```

TTTCTGAGATATCGCCTCAATTGTCCTGGCTGGGCTGTCGGGTCTGCCCGTTTTACAGATGGGCAAACTGGAGTGGGAAG
TATCCGGGTGGCTTCCTCAGGCCTGCAGCTGGTGGAGCAGCTACTGAAACAATCAGGAGCCCAGAAGCTTTGAAGTCACA
AGAAGAGAAGACTCCCAGA**ATG**CAGTGTGATGTTGGTGATGGACGCCTGTTTCGCCTTTCACTTAAACGTGCCCTTTCCA
GCTGCCCTGACCTCTTTGGGCTTTCCAGCCGCAACGAGCTGCTGGCCTCCTGCGGGAAGAAGTTCTGCAGCCGAGGGAGC
CGGTGCGTGCTCAGCAGGAAGACAGGGGAGCCCGAATGCCAGTGCCTGGAGGCATGCAGGCCCAGCTACGTGCCTGTGTG
CGGCTCTGATGGGAGGTTTTATGAAAACCACTGTAAGCTCCACCGTGCTGCTTGCCTCCTGGGAAAGAGGATCACCGTCA
TCCACAGCAAGGACTGTTTCCTCAAAGGTGACACGTGCACCATGGCCGGCTACGCCCGCTTGAAGAATGTCCTTCTGGCA
CTCCAGACCCGTCTGCAGCCACTCCAAGAAGGAGACAGCAGACAAGACCCTGCCTCCCAGAAGCGCCTCCTGGTGGAATC
TCTGTTCAGGGACTTAGATGCAGATGGCAATGGCCACCTCAGCAGCTCCGAACTGGCTCAGCATGTGCTGAAGAAGCAGG
ACCTGGATGAAGACTTACTTGGTTGCTCACCAGGTGACCTCCTCCGATTTGACGATTACAACAGTGACAGCTCCCTGACC
CTCCGCGAGTTCTACATGGCCTTCCAAGTGGTTCAGCTCAGCCTCGCCCCCGAGGACAGGGTCAGTGTGACCACAGTGAC
CGTGGGGCTGAGCACAGTGCTGACCTGCGCCGTCCATGGAGACCTGAGGCCACCAATCATCTGGAAGCGCAACGGGCTCA
CCCTGAACTTCCTGGACTTGGAAGACATCAATGACTTTGGAGAGGATGATTCCCTGTACATCACCAAGGTGACCACCATC
CACATGGGCAATTACACCTGCCATGCTTCCGGCCACGAGCAGCTGTTCCAGACCCACGTCCTGCAGGTGAATGTGCCGCC
AGTCATCCGTGTCTATCCAGAGAGCCAGGCACAGGAGCCTGGAGTGGCAGCCAGCCTAAGATGCCATGCTGAGGGCATTC
CCATGCCCAGAATCACTTGGCTGAAAAACGGCGTGGATGTCTCAACTCAGATGTCCAAACAGCTCTCCCTTTTAGCCAAT
GGGAGCGAACTCCACATCAGCAGTGTTCGGTATGAAGACACAGGGGCATACACCTGCATTGCCAAAAATGAAGTGGGTGT
GGATGAAGATATCTCCTCGCTCTTCATTGAAGACTCAGCTAGAAAGACCCTTGCAAACATCCTGTGGCGAGAGGAAGGCC
TCAGCGTGGGAAACATGTTCTATGTCTTCTCCGACGACGGTATCATCGTCATCCATCCTGTGGACTGTGAGATCCAGAGG
CACCTCAAACCCACGGAAAAGATTTTCATGAGCTATGAAGAAATCTGTCCTCAAAGAGAAAAAAATGCAACCCAGCCCTG
CCAGTGGGTATCTGCAGTCAATGTCCGGAACCGGTACATCTATGTGGCCCAGCCAGCACTGAGCAGAGTCCTTGTGGTCG
ACATCCAAGCCCAGAAAGTCCTACAGTCCATAGGTGTGGACCCTCTGCCGGCTAAGCTGTCCTATGACAAGTCACATGAC
CAAGTGTGGGTCCTGAGCTGGGGGGACGTGCACAAGTCCCGACCAAGTCTCCAGGTGATCACAGAAGCCAGCACCGGCCA
GAGCCAGCACCTCATCCGCACACCCTTTGCAGGAGTGGATGATTTCTTCATTCCCCCAACAAACCTCATCATCAACCACA
TCAGGTTTGGCTTCATCTTCAACAAGTCTGATCCTGCAGTCCACAAGGTGGACCTGGAAACAATGATGCCCCTCAAGACC
ATCGGCCTGCACCACCATGGCTGCGTGCCCCAGGCCATGGCACACACCCACCTGGGCGGCTACTTCTTCATCCAGTGCCG
ACAGGACAGCCCCGCCTCTGCTGCCCGACAGCTGCTCGTTGACAGTGTCACAGACTCTGTGCTTGGCCCCAATGGTGATG
TAACAGGCACCCCACACACATCCCCCGACGGGCGCTTCATAGTCAGTGCTGCAGCTGACAGCCCCTGGCTGCACGTGCAG
GAGATCACAGTGCGGGGCGAGATCCAGACCCTGTATGACCTGCAAATAAACTCGGGCATCTCAGACTTGGCCTTCCAGCG
CTCCTTCACTGAAAGCAATCAATACAACATCTACGCGGCTCTGCACACGGAGCCGGACCTGCTGTTCCTGGAGCTGTCCA
CGGGGAAGGTGGGCATGCTGAAGAACTTAAAGGAGCCACCCGCAGGGCCAGCTCAGCCCTGGGGGGTACCCACAGAATC
ATGAGGGACAGTGGGCTGTTTGGACAGTACCTCCTCACACCAGCCCGAGAGTCACTGTTCCTCATCAATGGGAGACAAAA
CACGCTGCGGTGTGAGGTGTCAGGTATAAAGGGGGGGACCACAGTGGTGTGGGTGGGTGAGGTA**TGA**AGGGCCCAGAGCA
GAGCCCTGGGCCAAGGAACACCCCCTAGTCCTGACACTGCAGCCTCAAGCAGGTACGCTGTACATTTTTACAGACAAAAG
CAAAAACCTGTACTCGCTTTGTGGTTCAACACTGGTCTCCTTGCAAGTTTCCTAGTATAAGGTATGCGCTGCTACCAAGA
TTGGGGTTTTTTCGTTAGGAAGTATGATTTATGCCTTGAGCTACGATGAGAACATATGCTGCTGTGTAAAGGGATCATTT
CTGTGCCAAGCTGCACACCGAGTGACCTGGGGACATCATGGAACCAAGGGATCCTGCTCTCCAAGCAGACACCTCTGTCA
GTTGCCTTCACATAGTCATTGTCCCTTACTGCCAGACCCAGCCAGACTTTGCCCTGACGGAGTGGCCCGGAAGCAGAGGC
CGACCAGGAGCAGGGGCCTCCCTCCCGAACTGAAAGCCCATCCGTCCTCGCGTGGGACCGCATCTTCTCCCTCGCAGCTG
CTTCTTGCTTTTCTTTCCATTTGACTTGCTGTAAGCCTGAGGGAGAGCCAACAAGACTTACTGCATCTTGGGGGATGGGG
AAATCACTCACTTTATTTTGGAAATTTTTGATTAAAAAAAAATTTTATAATCTCAAATGCTAGTAAGCAGAAAGATGCTC
TCCGAGGTCCAACTATATCCTTCCCTGCCTTAGGCCGAGTCTCGGGGGTGGTCACAACCCCACATCCCACAGCCAGAAAG
AACAATGGTCATCTGAGAATACTGGCCCTGTCGACTATTGCCACCCTGCTTCTCCAAGAGCAGACCAGGCCACCTCATCC
GTAAGGACTCGGTTCTGTGTTGGGACCCCAAAAAACCAGAACAAGTTCTGTGTGCCTCCTTTCAGCACAGAAGGGAGACA
TCTCATTAGTCAGGTCTGGTACCCCAGATTCAGGGCAGACTGGGCTTGCCTGGCAAGGTATGGGTGGCCTCCAGGCTCAA
TGCAGAAACCCCAAGGACACGAGTGGGGCCAGGTGAGTTCCTGAAGCTATACCTTTTCAAAACAGATTTTGTTTTCCTAC
CTGTGGCCCATCCACTCCTCTCTGGTACCCCATCCCCGCATCAGCACTGCAGAGAGAACACATTTCGGCGAGGGTTTTCT
TACCCACATTCCCCAATCAATACACACACACTGCAGAACCCAGAACAGAAGGCCACAGGCTGGCACTACTGCATTCTCCT
TATGTGTCTCAGGCTGTGGTGACTCTCACATGGGCATCGAAGAAGTACAACCCACATAGCCCTCTGGAGACCGCCTAGAT
CAGAGACTCAGCAAAAACAGGCTCGCCTTCCCTCTCCCACATATGAGTGGAACTTACATGTGTCCTGGTTTGAATGATCA
TTTTGCAAGCCACACGGGTTGGGAGAGGTGGTCTCACCACAGACGTCTTTGCTAATTTGGCCACCTTCACCTACTGACAT
GACCAGGATTTTCCTTTGCCATTAAGGAATGAACTCTTTCAAGGAGAGGAAACCCTAGACTCTGTGTCACTCTCAACACA
CACAGCTCCTTTCACTCCTGCCTGACTGCCAAGCCACCTGCATCCCCCGCCCCAGATCTCATGAGATCAATCACTTGTAT
GTCTCACGCAACTTGGTCCACCAAACGCCTGTCCCCTGTAACTCCTAGGGGTGCGCCTAGACAGGTACGTCTGTTTTTTA
TTTTAAAAGATATGCTATGTAGATATAAGTTGAGGAAGCTCACCTCAAAAGCCTAGAATGCAGTTTCACAGTAGCTGGGA
TGCATGGATGACCCATCTCACCCCTTTTTTTTTCCTGCCTCAATATCTTGATATGTTATGTTTACTCCCAATCTCCCATT
TTTACCACTAAAATTCTCCAACTTTCATAAACTTTTTTTGGAAAAATTTCCATTGTATCAGCCCCTGACAGAAAAAGGA
TCTCTGAGCCTAAAGGAGGAAAAGTCCCACCAACTACCAGACCAGAACACGAGCCCCTCTGGGCAGCAGGATTCCTAAGT
CAAAGACCAGTTTGACCCAAACTGGCCTTTTAAAATAATCAGGAGTGACAGAGTCAACTTCTGCAGCACCTGCTTCTCCC
CCACTGTCCCTTCCATCTTGGAATGTGTCTAAAAAAGCATAGCTGCCCTTTGCTGTCCTCAGAGTGCATTTCCTGGAGAC
GGCAGGCTTAGGTCTCACTGACAGCATGCCAGACACAACTGAATCGAAGCAGGCCTGAAGCCTAGGTCAGGGTTTCAGGA
GTCCAGCCCCAGGAGGCAAAGTCACCAATGCAGGGAGGTAAATGCCTTTTGGCAGGAAAACCAATAGAGTTGGTTGGGTG
GGGAGTCAGGGGTGGAGGAGAAGGAGGAAGAGGAGGAAGGCCAGACTGGCCTGCCCTTTCTCCCATACTTCACCCCAGC
AGAGGTTCATGGGACACAGTTGGAAAGCCACTGGGAGGAAATGCCTCACTACAGGGGGGCCTCCTGTAGCAAGCCCAGCC
GGTAATCCTCCTAATGAACCCACAAGGTCAATTCACAACTGATATCTTAGCTATTAAAGAAGTACTGACTTTACCAAAAG
AATCATCAAGAAAGCTATTTATATAAACCCCCTCAGTCATTTTGAAATAAAATTAATTTTAC

The predicted amino acid sequence of FCTR2 protein corresponding to the foregoing nucleotide sequence is reported in Table 2B. FCTR2 was searched against other databases using SignalPep and PSort search protocols. The protein is most likely located in the mitochondrial matrix space (certainty=0.4718) and seems to have no N-terminal signal sequence. The predicted molecular weight is 90346.9 Daltons.

Table 2B. FCTR2 Protein Sequence (SEQ ID NO:4).

```
MQCDVGDGRLFRLSLKRALSSCPDLFGLSSRNELLASCGKKFCSRGSRCVLSRKTGEPECQCLEACRPSYVPVCGSDGRFYENHCK
LHRAACLLGKRITVIHSKDCFLKGDTCTMAGYARLKNVLLALQTRLQPLQEGDSRQDPASQKRLLVESLFRDLDADGNGHLSSSEL
AQHVLKKQDLDEDLLGCSPGDLLRFDDYNSDSSLTLREFYMAFQVVQLSLAPEDRVSVTTVTVGLSTVLTCAVHGDLRPPIIWKRN
GLTLNFLDLEDINDFGEDDSLYITKVTTIHMGNYTCHASGHEQLFQTHVLQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPR
ITWLKNGVDVSTQMSKQLSLLANGSELHISSVRYEDTGAYTCIAKNEVGVDEDISSLFIEDSARKTLANILWREEGLSVGNMFYVF
SDDGIIVIHPVDCEIQRHLKPTEKIFMSYEEICPQREKNATQPCQWVSAVNVRNRYIYVAQPALSRVLVVDIQAQKVLQSIGVDPL
PAKLSYDKSHDQVWVLSWGDVHKSRPSLQVITEASTGQSQHLIRTPFAGVDDFFIPPTNLIINHIRFGFIFNKSDPAVHKVDLETM
MPLKTIGLHHHGCVPQAMAHTHLGGYFFIQCRQDSPASAARQLLVDSVTDSVLGPNGDVTGTPHTSPDGRFIVSAAADSPWLHVQE
ITVRGEIQTLYDLQINSGISDLAFQRSFTESNQYNIYAALHTEPDLLFLELSTGKVGMLKNLKEPPAGPAQPWGGTHRIMRDSGLF
GQYLLTPARESLFLINGRQNTLRCEVSGIKGGTTVVWVGEV
```

In a BLASTN search it was also found that nucleotides 784-5502 of FCTR2 nucleic acid had 4672 of 4719 bases (99%) identical to *Homo sapiens* mRNA for KIAA1061 protein, partial cds (GenBank Acc:AB028984) (Table 2C).

Table 2C. BLASTN of FCTR2 against *Homo sapiens* mRNA for KIAA1061 protein (SEQ ID NO:46)

```
>GI|5689458|DBJ|AB028984.1|AB028984 HOMO SAPIENS MRNA FOR KIAA1061 PROTEIN, PARTIAL
CDS
          LENGTH = 4719

 SCORE = 9075 BITS (4578), EXPECT = 0.0
 IDENTITIES = 4672/4719 (99%)
 STRAND = PLUS / PLUS

QUERY: 784   AGAATGTCCTTCTGGCACTCCAGACCCGTCTGCAGCCACTCCAAGAAGGAGACAGCAGAC 843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1     AGAATGTCCTTCTGGCACTCCAGACCCGTCTGCAGCCACTCCAAGAAGGAGACAGCAGAC 60

QUERY: 844   AAGACCCTGCCTCCCAGAAGCGCCTCCTGGTGGAATCTCTGTTCAGGGACTTAGATGCAG 903
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 61    AAGACCCTGCCTCCCAGAAGCGCCTCCTGGTGGAATCTCTGTTCAGGGACTTAGATGCAG 120

QUERY: 904   ATGGCAATGGCCACCTCAGCAGCTCCGAACTGGCTCAGCATGTGCTGAAGAAGCAGGACC 963
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 121   ATGGCAATGGCCACCTCAGCAGCTCCGAACTGGCTCAGCATGTGCTGAAGAAGCAGGACC 180

QUERY: 964   TGGATGAAGACTTACTTGGTTGCTCACCAGGTGACCTCCTCCGATTTGACGATTACAACA 1023
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 181   TGGATGAAGACTTACTTGGTTGCTCACCAGGTGACCTCCTCCGATTTGACGATTACAACA 240

QUERY: 1024  GTGACAGCTCCCTGACCCTCCGCGAGTTCTACATGGCCTTCCAAGTGGTTCAGCTCAGCC 1083
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 241   GTGACAGCTCCCTGACCCTCCGCGAGTTCTACATGGCCTTCCAAGTGGTTCAGCTCAGCC 300

QUERY: 1084  TCGCCCCCGAGGACAGGGTCAGTGTGACCACAGTGACCGTGGGGCTGAGCACAGTGCTGA 1143
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 301   TCGCCCCCGAGGACAGGGTCAGTGTGACCACAGTGACCGTGGGGCTGAGCACAGTGCTGA 360
```

```
QUERY: 1144 CCTGCGCCGTCCATGGAGACCTGAGGCCACCAATCATCTGGAAGCGCAACGGGCTCACCC 1203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 361  CCTGCGCCGTCCATGGAGACCTGAGGCCACCAATCATCTGGAAGCGCAACGGGCTCACCC 420

QUERY: 1204 TGAACTTCCTGGACTTGGAAGACATCAATGACTTTGGAGAGGATGATTCCCTGTACATCA 1263
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 421  TGAACTTCCTGGACTTGGAAGACATCAATGACTTTGGAGAGGATGATTCCCTGTACATCA 480

QUERY: 1264 CCAAGGTGACCACCATCCACATGGGCAATTACACCTGCCATGCTTCCGGCCACGAGCAGC 1323
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 481  CCAAGGTGACCACCATCCACATGGGCAATTACACCTGCCATGCTTCCGGCCACGAGCAGC 540

QUERY: 1324 TGTTCCAGACCCACGTCCTGCAGGTGAATGTGCCGCCAGTCATCCGTGTCTATCCAGAGA 1383
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 541  TGTTCCAGACCCACGTCCTGCAGGTGAATGTGCCGCCAGTCATCCGTGTCTATCCAGAGA 600

QUERY: 1384 GCCAGGCACAGGAGCCTGGAGTGGCAGCCAGCCTAAGATGCCATGCTGAGGGCATTCCCA 1443
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 601  GCCAGGCACAGGAGCCTGGAGTGGCAGCCAGCCTAAGATGCCATGCTGAGGGCATTCCCA 660

QUERY: 1444 TGCCCAGAATCACTTGGCTGAAAAACGGCGTGGATGTCTCAACTCAGATGTCCAAACAGC 1503
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 661  TGCCCAGAATCACTTGGCTGAAAAACGGCGTGGATGTCTCAACTCAGATGTCCAAACAGC 720

QUERY: 1504 TCTCCCTTTTAGCCAATGGGAGCGAACTCCACATCAGCAGTGTTCGGTATGAAGACACAG 1563
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 721  TCTCCCTTTTAGCCAATGGGAGCGAACTCCACATCAGCAGTGTTCGGTATGAAGACACAG 780

QUERY: 1564 GGGCATACACCTGCATTGCCAAAAATGAAGTGGGTGTGGATGAAGATATCTCCTCGCTCT 1623
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 781  GGGCATACACCTGCATTGCCAAAAATGAAGTGGGTGTGGATGAAGATATCTCCTCGCTCT 840

QUERY: 1624 TCATTGAAGACTCAGCTAGAAAGACCCTTGCAAACATCCTGTGGCGAGAGGAAGGCCTCA 1683
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 841  TCATTGAAGACTCAGCTAGAAAGACCCTTGCAAACATCCTGTGGCGAGAGGAAGGCCTCA 900

QUERY: 1684 GCGTGGGAAACATGTTCTATGTCTTCTCCGACGACGGTATCATCGTCATCCATCCTGTGG 1743
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 901  GCGTGGGAAACATGTTCTATGTCTTCTCCGACGACGGTATCATCGTCATCCATCCTGTGG 960

QUERY: 1744 ACTGTGAGATCCAGAGGCACCTCAAACCCACGGAAAAGATTTTCATGAGCTATGAAGAAA 1803
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 961  ACTGTGAGATCCAGAGGCACCTCAAACCCACGGAAAAGATTTTCATGAGCTATGAAGAAA 1020

QUERY: 1804 TCTGTCCTCAAAGAGNNNNNNNTGCAACCCAGCCCTGCCAGTGGGTATCTGCAGTCAATG 1863
            |||||||||||||||       ||||||||||||||||||||||||||||||||||||||
SBJCT: 1021 TCTGTCCTCAAAGAGAAAAAAATGCAACCCAGCCCTGCCAGTGGGTATCTGCAGTCAATG 1080

QUERY: 1864 TCCGGAACCGGTACATCTATGTGGCCCAGCCAGCACTGAGCAGAGTCCTTGTGGTCGACA 1923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1081 TCCGGAACCGGTACATCTATGTGGCCCAGCCAGCACTGAGCAGAGTCCTTGTGGTCGACA 1140

QUERY: 1924 TCCAAGCCCAGAAAGTCCTACAGTCCATAGGTGTGGACCCTCTGCCGGCTAAGCTGTCCT 1983
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1141 TCCAAGCCCAGAAAGTCCTACAGTCCATAGGTGTGGACCCTCTGCCGGCTAAGCTGTCCT 1200

QUERY: 1984 ATGACAAGTCACATGACCAAGTGTGGGTCCTGAGCTGGGGGGACGTGCACAAGTCCCGAC 2043
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1201 ATGACAAGTCACATGACCAAGTGTGGGTCCTGAGCTGGGGGGACGTGCACAAGTCCCGAC 1260

QUERY: 2044 CAAGTCTCCAGGTGATCACAGAAGCCAGCACCGGCCAGAGCCAGCACCTCATCCGCACAC 2103
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1261 CAAGTCTCCAGGTGATCACAGAAGCCAGCACCGGCCAGAGCCAGCACCTCATCCGCACAC 1320

QUERY: 2104 CCTTTGCAGGAGTGGATGATTTCTTCATTCCCCCAACAAACCTCATCATCAACCACATCA 2163
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1321 CCTTTGCAGGAGTGGATGATTTCTTCATTCCCCCAACAAACCTCATCATCAACCACATCA 1380

QUERY: 2164 GGTTTGGCTTCATCTTCAACAAGTCTGATCCTGCAGTCCACAAGGTGGACCTGGAAACAA 2223
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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SBJCT: 1381 GGTTTGGCTTCATCTTCAACAAGTCTGATCCTGCAGTCCACAAGGTGGACCTGGAAACAA 1440

QUERY: 2224 TGATGCCCCTCAAGACCATCGGCCTGCACCACCATGGCTGCGTGCCCCAGGCCATGGCAC 2283
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1441 TGATGCCCCTCAAGACCATCGGCCTGCACCACCATGGCTGCGTGCCCCAGGCCATGGCAC 1500

QUERY: 2284 ACACCCACCTGGGCGGCTACTTCTTCATCCAGTGCCGACAGGACAGCCCCGCCTCTGCTG 2343
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1501 ACACCCACCTGGGCGGCTACTTCTTCATCCAGTGCCGACAGGACAGCCCCGCCTCTGCTG 1560

QUERY: 2344 CCCGACAGCTGCTCGTTGACAGTGTCACAGACTCTGTGCTTGGCCCCAATGGTGATGTAA 2403
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1561 CCCGACAGCTGCTCGTTGACAGTGTCACAGACTCTGTGCTTGGCCCCAATGGTGATGTAA 1620

QUERY: 2404 CAGGCACCCCACACACATCCCCCGACGGGCGCTTCATAGTCAGTGCTGCAGCTGACAGCC 2463
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1621 CAGGCACCCCACACACATCCCCCGACGGGCGCTTCATAGTCAGTGCTGCAGCTGACAGCC 1680

QUERY: 2464 CCTGGCTGCACGTGCAGGAGATCACAGTGCGGGGCGAGATCCAGACCCTGTATGACCTGC 2523
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1681 CCTGGCTGCACGTGCAGGAGATCACAGTGCGGGGCGAGATCCAGACCCTGTATGACCTGC 1740

QUERY: 2524 AAATAAACTCGGGCATCTCAGACTTGGCCTTCCAGCGCTCCTTCACTGAAAGCAATCAAT 2583
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1741 AAATAAACTCGGGCATCTCAGACTTGGCCTTCCAGCGCTCCTTCACTGAAAGCAATCAAT 1800

QUERY: 2584 ACAACATCTACGCGGCTCTGCACACGGAGCCGGACCTGCTGTTCCTGGAGCTGTCCACGG 2643
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1801 ACAACATCTACGCGGCTCTGCACACGGAGCCGGACCTGCTGTTCCTGGAGCTGTCCACGG 1860

QUERY: 2644 GGAAGGTGGGCATGCTGAAGAACTTAAAGGAGCCACCCGCAGGGCCAGCTCAGCCCTNNN 2703
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1861 GGAAGGTGGGCATGCTGAAGAACTTAAAGGAGCCACCCGCAGGGCCAGCTCAGCCCTGGG 1920

QUERY: 2704 NNNNTACCCACAGAATCATGAGGGACAGTGGGCTGTTTGGACAGTACCTCCTCACACCAG 2763
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1921 GGGGTACCCACAGAATCATGAGGGACAGTGGGCTGTTTGGACAGTACCTCCTCACACCAG 1980

QUERY: 2764 CCCGAGAGTCACTGTTCCTCATCAATGGGAGACAAAACACGCTGCGGTGTGAGGTGTCAG 2823
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1981 CCCGAGAGTCACTGTTCCTCATCAATGGGAGACAAAACACGCTGCGGTGTGAGGTGTCAG 2040

QUERY: 2824 GTATAAANNNNNNACCACAGTGGTGTGGGTGGGTGAGGTATGAAGGGCCCAGAGCAGAG 2883
            |||||||      ||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2041 GTATAAAGGGGGGGACCACAGTGGTGTGGGTGGGTGAGGTATGAAGGGCCCAGAGCAGAG 2100

QUERY: 2884 CCCTGGGCCAAGGAACACCCCCCTAGTCCTGACACTGCAGCCTCAAGCAGGTACGCTGTAC 2943
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2101 CCCTGGGCCAAGGAACACCCCCCTAGTCCTGACACTGCAGCCTCAAGCAGGTACGCTGTAC 2160

QUERY: 2944 ATTTTTACAGACAAAAGCAAAAACCTGTACTCGCTTTGTGGTTCAACACTGGTCTCCTTG 3003
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2161 ATTTTTACAGACAAAAGCAAAAACCTGTACTCGCTTTGTGGTTCAACACTGGTCTCCTTG 2220

QUERY: 3004 CAAGTTTCCTAGTATAAGGTATGCGCTGCTACCAAGATTGGGGTTTTTTCGTTAGGAAGT 3063
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2221 CAAGTTTCCTAGTATAAGGTATGCGCTGCTACCAAGATTGGGGTTTTTTCGTTAGGAAGT 2280

QUERY: 3064 ATGATTTATGCCTTGAGCTACGATGAGAACATATGCTGCTGTGTAAAGGGATCATTTCTG 3123
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2281 ATGATTTATGCCTTGAGCTACGATGAGAACATATGCTGCTGTGTAAAGGGATCATTTCTG 2340

QUERY: 3124 TGCCAAGCTGCACACCGAGTGACCTGGGGACATCATGGAACCAAGGGATCCTGCTCTCCA 3183
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2341 TGCCAAGCTGCACACCGAGTGACCTGGGGACATCATGGAACCAAGGGATCCTGCTCTCCA 2400

QUERY: 3184 AGCAGACACCTCTGTCAGTTGCCTTCACATAGTCATTGTCCCTTACTGCCAGACCCAGCC 3243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2401 AGCAGACACCTCTGTCAGTTGCCTTCACATAGTCATTGTCCCTTACTGCCAGACCCAGCC 2460
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QUERY: 3244 AGACTTTGCCCTGACGGAGTGGCCCGGAAGCAGAGGCCGACCAGGAGCAGGGGCCTCCCT 3303
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2461 AGACTTTGCCCTGACGGAGTGGCCCGGAAGCAGAGGCCGACCAGGAGCAGGGGCCTCCCT 2520

QUERY: 3304 CCCGAACTGAAAGCCCATCCGTCCTCGCGTGGGACCGCATCTTCTCCCTCGCAGCTGCTT 3363
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2521 CCCGAACTGAAAGCCCATCCGTCCTCGCGTGGGACCGCATCTTCTCCCTCGCAGCTGCTT 2580

QUERY: 3364 CTTGCTTTTCTTTCCATTTGACTTGCTGTAAGCCTGAGGGAGAGCCAACAAGACTTACTG 3423
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2581 CTTGCTTTTCTTTCCATTTGACTTGCTGTAAGCCTGAGGGAGAGCCAACAAGACTTACTG 2640

QUERY: 3424 CATCTTGGGGGATGGGGAAATCACTCACTTTATTTGGAAATTTTTGATTNNNNNNNNNNT 3483
            |||||||||||||||||||||||||||||||||||||||||||||||||          |
SBJCT: 2641 CATCTTGGGGGATGGGGAAATCACTCACTTTATTTGGAAATTTTTGATTAAAAAAAAAAT 2700

QUERY: 3484 TTTATAATCTCAAATGCTAGTAAGCAGAAAGATGCTCTCCGAGGTCCAACTATATCCTTC 3543
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2701 TTTATAATCTCAAATGCTAGTAAGCAGAAAGATGCTCTCCGAGGTCCAACTATATCCTTC 2760

QUERY: 3544 CCTGCCTTAGGCCGAGTCTCGGGGGTGGTCACAACCCCACATCCCACAGCCAGAAAGAAC 3603
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2761 CCTGCCTTAGGCCGAGTCTCGGGGGTGGTCACAACCCCACATCCCACAGCCAGAAAGAAC 2820

QUERY: 3604 AATGGTCATCTGAGAATACTGGCCCTGTCGACTATTGCCACCCTGCTTCTCCAAGAGCAG 3663
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2821 AATGGTCATCTGAGAATACTGGCCCTGTCGACTATTGCCACCCTGCTTCTCCAAGAGCAG 2880

QUERY: 3664 ACCAGGCCACCTCATCCGTAAGGACTCGGTTCTGTGTTGGGACCCCAAAAAACCAGAACA 3723
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2881 ACCAGGCCACCTCATCCGTAAGGACTCGGTTCTGTGTTGGGACCCCAAAAAACCAGAACA 2940

QUERY: 3724 AGTTCTGTGTGCCTCCTTTCAGCACAGAAGGGAGACATCTCATTAGTCAGGTCTGGTACC 3783
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2941 AGTTCTGTGTGCCTCCTTTCAGCACAGAAGGGAGACATCTCATTAGTCAGGTCTGGTACC 3000

QUERY: 3784 CCAGATTCAGGGCAGACTGGGCTTGCCTGGCAAGGTATGGGTGGCCTCCAGGCTCAATGC 3843
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3001 CCAGATTCAGGGCAGACTGGGCTTGCCTGGCAAGGTATGGGTGGCCTCCAGGCTCAATGC 3060

QUERY: 3844 AGAAACCCCAAGGACACGAGTGGGGCCAGGTGAGTTCCTGAAGCTATACCTTTTCAAAAC 3903
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3061 AGAAACCCCAAGGACACGAGTGGGGCCAGGTGAGTTCCTGAAGCTATACCTTTTCAAAAC 3120

QUERY: 3904 AGATTTTGTTTTCCTACCTGTGGCCCATCCACTCCTCTCTGGTACCCCATCCCCGCATCA 3963
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3121 AGATTTTGTTTTCCTACCTGTGGCCCATCCACTCCTCTCTGGTACCCCATCCCCGCATCA 3180

QUERY: 3964 GCACTGCAGAGAGAACACATTTCGGCGAGGGTTTTCTTACCCACATTCCCCAATCAATAC 4023
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3181 GCACTGCAGAGAGAACACATTTCGGCGAGGGTTTTCTTACCCACATTCCCCAATCAATAC 3240

QUERY: 4024 ACACACACTGCAGAACCCAGAACAGAAGGCCACAGGCTGGCACTACTGCATTCTCCTTAT 4083
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3241 ACACACACTGCAGAACCCAGAACAGAAGGCCACAGGCTGGCACTACTGCATTCTCCTTAT 3300

QUERY: 4084 GTGTCTCAGGCTGTGGTGACTCTCACATGGGCATCGAAGAAGTACAACCCACATAGCCCT 4143
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3301 GTGTCTCAGGCTGTGGTGACTCTCACATGGGCATCGAAGAAGTACAACCCACATAGCCCT 3360

QUERY: 4144 CTGGAGACCGCCTAGATCAGAGACTCAGCAAAAACAGGCTCGCCTTCCCTCTCCCACATA 4203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3361 CTGGAGACCGCCTAGATCAGAGACTCAGCAAAAACAGGCTCGCCTTCCCTCTCCCACATA 3420

QUERY: 4204 TGAGTGGAACTTACATGTGTCCTGGTTTGAATGATCATTTTGCAAGCCACACGGGTTGGG 4263
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3421 TGAGTGGAACTTACATGTGTCCTGGTTTGAATGATCATTTTGCAAGCCACACGGGTTGGG 3480

QUERY: 4264 AGAGGTGGTCTCACCACAGACGTCTTTGCTAATTTGGCCACCTTCACCTACTGACATGAC 4323
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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SBJCT: 3481 AGAGGTGGTCTCACCACAGACGTCTTTGCTAATTTGGCCACCTTCACCTACTGACATGAC 3540

QUERY: 4324 CAGGATTTTCCTTTGCCATTAAGGAATGAACTCTTTCAAGGAGAGGAAACCCTAGACTCT 4383
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3541 CAGGATTTTCCTTTGCCATTAAGGAATGAACTCTTTCAAGGAGAGGAAACCCTAGACTCT 3600

QUERY: 4384 GTGTCACTCTCAACACACACAGCTCCTTTCACTCCTGCCTGACTGCCAAGCCACCTGCAT 4443
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3601 GTGTCACTCTCAACACACACAGCTCCTTTCACTCCTGCCTGACTGCCAAGCCACCTGCAT 3660

QUERY: 4444 CCCCCGCCCCAGATCTCATGAGATCAATCACTTGTATGTCTCACGCAACTTGGTCCACCA 4503
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3661 CCCCCGCCCCAGATCTCATGAGATCAATCACTTGTATGTCTCACGCAACTTGGTCCACCA 3720

QUERY: 4504 AACGCCTGTCCCCTGTAACTCCTAGGGGTGCGCCTAGACAGGTACGTCTGTTTTTTATTT 4563
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3721 AACGCCTGTCCCCTGTAACTCCTAGGGGTGCGCCTAGACAGGTACGTCTGTTTTTTATTT 3780

QUERY: 4564 TAAAAGATATGCTATGTAGATATAAGTTGAGGAAGCTCACCTCAAAAGCCTAGAATGCAG 4623
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3781 TAAAAGATATGCTATGTAGATATAAGTTGAGGAAGCTCACCTCAAAAGCCTAGAATGCAG 3840

QUERY: 4624 TTTCACAGTAGCTGGGATGCATGGATGACCCATCTCACCCCNNNNNNNNNCCTGCCTCAA 4683
            |||||||||||||||||||||||||||||||||||||||||         ||||||||||
SBJCT: 3841 TTTCACAGTAGCTGGGATGCATGGATGACCCATCTCACCCCTTTTTTTTTCCTGCCTCAA 3900

QUERY: 4684 TATCTTGATATGTTATGTTTACTCCCAATCTCCCATTTTTACCACTAAAATTCTCCAACT 4743
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3901 TATCTTGATATGTTATGTTTACTCCCAATCTCCCATTTTTACCACTAAAATTCTCCAACT 3960

QUERY: 4744 TTCATAAACNNNNNNNNGGAAAAATTTCCATTGTATCAGCCCCTGACAGAAAAAGGATCT 4803
            |||||||||        |||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3961 TTCATAAACTTTTTTTTGGAAAAATTTCCATTGTATCAGCCCCTGACAGAAAAAGGATCT 4020

QUERY: 4804 CTGAGCCTAAAGGAGGAAAAGTCCCACCAACTACCAGACCAGAACACGAGCCCCTCTGGG 4863
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4021 CTGAGCCTAAAGGAGGAAAAGTCCCACCAACTACCAGACCAGAACACGAGCCCCTCTGGG 4080

QUERY: 4864 CAGCAGGATTCCTAAGTCAAAGACCAGTTTGACCCAAACTGGCCTTTTAAAATAATCAGG 4923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4081 CAGCAGGATTCCTAAGTCAAAGACCAGTTTGACCCAAACTGGCCTTTTAAAATAATCAGG 4140

QUERY: 4924 AGTGACAGAGTCAACTTCTGCAGCACCTGCTTCTCCCCCACTGTCCCTTCCATCTTGGAA 4983
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4141 AGTGACAGAGTCAACTTCTGCAGCACCTGCTTCTCCCCCACTGTCCCTTCCATCTTGGAA 4200

QUERY: 4984 TGTGTCTAAAAAAGCATAGCTGCCCTTTGCTGTCCTCAGAGTGCATTTCCTGGAGACGGC 5043
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4201 TGTGTCTAAAAAAGCATAGCTGCCCTTTGCTGTCCTCAGAGTGCATTTCCTGGAGACGGC 4260

QUERY: 5044 AGGCTTAGGTCTCACTGACAGCATGCCAGACACAACTGAATCGAAGCAGGCCTGAAGCCT 5103
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4261 AGGCTTAGGTCTCACTGACAGCATGCCAGACACAACTGAATCGAAGCAGGCCTGAAGCCT 4320

QUERY: 5104 AGGTCAGGGTTTCAGGAGTCCAGCCCCAGGAGGCAAAGTCACCAATGCAGGGAGGTAAAT 5163
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4321 AGGTCAGGGTTTCAGGAGTCCAGCCCCAGGAGGCAAAGTCACCAATGCAGGGAGGTAAAT 4380

QUERY: 5164 GCCTTTTGGCAGGAAAACCAATAGAGTTGGTTGGGTGGGGAGTCAGGGGTGGAGGAGAA 5223
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4381 GCCTTTTGGCAGGAAAACCAATAGAGTTGGTTGGGTGGGGAGTCAGGGGTGGAGGAGAA 4440

QUERY: 5224 GGAGGAAGAGGAGGAAGGCCAGACTGGCCTGCCCTTTCTCCCATACTTCACCCCAGCAGA 5283
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4441 GGAGGAAGAGGAGGAAGGCCAGACTGGCCTGCCCTTTCTCCCATACTTCACCCCAGCAGA 4500

QUERY: 5284 GGTTCATGGGACACAGTTGGAAAGCCACTGGGAGGAAATGCCTCACTACAGGGGGGCCTC 5343
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4501 GGTTCATGGGACACAGTTGGAAAGCCACTGGGAGGAAATGCCTCACTACAGGGGGGCCTC 4560
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QUERY: 5344 CTGTAGCAAGCCCAGCCGGTAATCCTCCTAATGAACCCACAAGGTCAATTCACAACTGAT 5403
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4561 CTGTAGCAAGCCCAGCCGGTAATCCTCCTAATGAACCCACAAGGTCAATTCACAACTGAT 4620

QUERY: 5404 ATCTTAGCTATTAAAGAAGTACTGACTTTACCAAAAGAATCATCAAGAAAGCTATTTATA 5463
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4621 ATCTTAGCTATTAAAGAAGTACTGACTTTACCAAAAGAATCATCAAGAAAGCTATTTATA 4680

QUERY: 5464 TAAACCCCCTCAGTCATTTTGAAATAAAATTAATTTTAC 5502
            |||||||||||||||||||||||||||||||||||||||
SBJCT: 4681 TAAACCCCCTCAGTCATTTTGAAATAAAATTAATTTTAC 4719
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The FCTR2 amino acid sequence has 473 of 810 amino acid residues (58%) identical to, and 616 of 810 residues (76%) positive with, the 850 amino acid residue proteins from *Homo sapiens* KIAA1263 Protein fragment (ptnr: TREMBLNEW-ACC:BAA86577) (SEQ ID NO:47) (Table 2D).

Table 2D. BLASTP of FCTR2 against *Homo sapiens* KIAA1263 Protein fragment (SEQ ID NO:47)

ptnr:TREMBLNEW-ACC:BAA86577 KIAA1263 PROTEIN - Homo sapiens (Human), 850 aa (fragment)

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  Length = 850

 Score = 2573 (905.7 bits), Expect = 2.0e-267, P = 2.0e-267
 Identities = 473/810 (58%), Positives = 616/810 (76%)

QUERY: 10  LFRLSLKRALSSCPDLFGLSSRNELLASCGKKFCSRGSRCVLSRKTGEPECQCLEACRPS 69
           | ||  |        + |   ++    ||  |+|  |  || ||+||+ || |++ |+
SBJCT: 40  LMRLRHKEKNQESSRVKGFMIQDGPFGSCENKYCGLGRHCVTSRETGQAECACMDLCKRH 99

QUERY: 70  YVPVCGSDGRFYENHCKLHRAACLLGKRITVIHSKDCFLKGDTCTMAGYARLKNVLLALQ 129
           | ||||||| ||||||++||||||  ++||++|++||| ||| |    |+++||+|| ||
SBJCT: 100 YKPVCGSDGEFYENHCEVHRAACLKKQKITIVHNEDCFFKGDKCKTTEYSKMKNMLLDLQ 159

QUERY: 130 TRLQPLQEGDSRQ-DPASQKRLLVESLFRDLDADGNGHLSSSELAQHVLKKQDLDEDLLG 188
            +   +|| ++   |  |+|+|||+ +|+  ||| || +  +|| | |+|+++| +||
SBJCT: 160 NQKYIMQENENPNGDDISRKKLLVDQMFKYFDADSNGLVDINELTQ-VIKQEELGKDLFD 218

QUERY: 189 CSPGDLLRFDDYNSDSSLTLREFYMAFQVVQLSLAPEDRVSVTTVTVGLSTVLTCAVHGD 248
           |+   ||++||+|+|  | | ||| ||||+||||  + + | |  ||| | || ||+ |
SBJCT: 219 CTLYVLLKYDDFNADKHLALEEFYRAFQVIQLSLPEDQKLSITAATVGQSAVLSCAIQGT 278

QUERY: 249 LRPPIIWKRNGLTLNFLDLEDINDFGEDDSLYITKVTTIHMGNYTCHASGHEQLFQTHVL 308
           |||||||||| + || ||||||||||+| ||||||||| |+|||||+| |+||++|||+
SBJCT: 279 LRPPIIWKRNNIILNNLDLEDINDFGDDGSLYITKVTTTHVGNYTCYADGYEQVYQTHIF 338

QUERY: 309 QVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITWLKNGVDVSTQMSKQLSLLANG 368
           ||||||||||||||||+|||| ||||||||||| |++ |||||+|++ ++||||+| |||
SBJCT: 339 QVNVPPVIRVYPESQAREPGVTASLRCHAEGIPKPQLGWLKNGIDITPKLSKQLTLQANG 398

QUERY: 369 SELHISSVRYEDTGAYTCIAKNEVGVDEDISSLFIEDSARKTLANILWREEGLSVGNMFY 428
           ||+|||+|||||||||||||||| ||||||||||+|||||||||||||||||| +|||||
SBJCT: 399 SEVHISNVRYEDTGAYTCIAKNEAGVDEDISSLFVEDSARKTLANILWREEGLGIGNMFY 458

QUERY: 429 VFSDDGIIVIHPVDCEIQRHLKPTEKIFMSYEEICPQREKNATQPCQWVSAVNVRNRYIY 488
           || +||| || |++|| |||+||+||+    +|+||+ | +  | | | |||||++++||
SBJCT: 459 VFYEDGIKVIQPIECEFQRHIKPSEKLLGFQDEVCPKAEGDEVQRCVWASAVNVKDKFIY 518

QUERY: 489 VAQPALSRVLVVDIQAQKVLQSIGVDPLPAKLSYDKSHDQVWVLSWGDVHKSRPSLQVIT 548
           |||| | |||+||+|+|||+|++  ||+| || |||||||||||||| + |+ |+|||||
SBJCT: 519 VAQPTLDRVLIVDVQSQKVVQAVSTDPVPVKLHYDKSHDQVWVLSWGTLEKTSPTLQVIT 578

QUERY: 549 EASTGQSQHLIRT-----PFAGVDDFFIPPTNLIINHIRFGFIFNKSDPAVHKVDLETMM 603
```

```
            ||     | | |      |  ||||||| | ||| |+||||| +| + |+ |+|||||
SBJCT: 579 LASGNVPHHTIHTQPVGKQFDRVDDFFIPTTTLIITHMRFGFILHKDEAALQKIDLETMS 638

QUERY: 604 PLKTIGLHHHGCVPQAMAHTHLGGYFFIQCRQDSPASAARQLLVDSVTDSVLGPNGDVTG 663
            +||| |  + ||||++|+||||||+|| |+ ||  + + |++|| |||||+| | ||||
SBJCT: 639 YIKTINLKDYKCVPQSLAYTHLGGYYFIGCKPDSTGAVSPQVMVDGVTDSVIGFNSDVTG 698

QUERY: 664 TPHTSPDGRFIVSAAADSPWLHVQEITVRGEIQTLYDLQINSGISDLAFQRSFTESNQYN 723
           ||+ |||| ++||       + || ||+|||||  +|+  |  ||||||| ||||++|||
SBJCT: 699 TPYVSPDGHYLVSINDVKGLVRVQYITIRGEIQEAFDIYTNLHISDLAFQPSFTEAHQYN 758

QUERY: 724 IYAALHTEPDLLFLELSTGKVGMLKNLKEPPAGPAQPWGGTHRIMRDSGLFGQYLLTPAR 783
           || +  |+ |+||+|||+||| |+|+||||      ||   +| ++|||||||||+||++
SBJCT: 759 IYGSSSTQTDVLFVELSSGKVKMIKSLKEPLKAEEWPWNRKNRQIQDSGLFGQYLMTPSK 818

QUERY: 784 ESLFLINGRQNTLRCEVSGIKGGTTVVWVGE 814
           +|||+++|| | | ||++ ++ | ||+|||+
SBJCT: 819 DSLFILDGRLNKLNCEITEVEKGNTVIWVGD 849
```

Amino acids 123-815 of FCTR2 also have 693 of 693 amino acid residues (100%) identical to,the 693 amino acid residue protein fragment of KIAA1061 Protein from *Homo sapiens* (ptnr: TREMBLNEW-ACC: BAA83013) (SEQ ID NO:48) (Table 2E).

Table 2E. BLASTP of FCTR2 against KIAA1061 Protein [Fragment] (SEQ ID NO:48)

```
ptnr:TREMBLNEW-ACC:BAA83013 KIAA1061 PROTEIN - Homo sapiens (Human),
693 aa (fragment).
          Length = 693

 Score = 3623 (1275.4 bits), Expect = 0.0, P = 0.0
 Identities = 693/693 (100%), Positives = 693/693 (100%)

QUERY: 123 NVLLALQTRLQPLQEGDSRQDPASQKRLLVESLFRDLDADGNGHLSSSELAQHVLKKQDL 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1   NVLLALQTRLQPLQEGDSRQDPASQKRLLVESLFRDLDADGNGHLSSSELAQHVLKKQDL 60

QUERY: 183 DEDLLGCSPGDLLRFDDYNSDSSLTLREFYMAFQVVQLSLAPEDRVSVTTVTVGLSTVLT 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 61  DEDLLGCSPGDLLRFDDYNSDSSLTLREFYMAFQVVQLSLAPEDRVSVTTVTVGLSTVLT 120

QUERY: 243 CAVHGDLRPPIIWKRNGLTLNFLDLEDINDFGEDDSLYITKVTTIHMGNYTCHASGHEQL 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 121 CAVHGDLRPPIIWKRNGLTLNFLDLEDINDFGEDDSLYITKVTTIHMGNYTCHASGHEQL 180

QUERY: 303 FQTHVLQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITWLKNGVDVSTQMSKQL 362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 181 FQTHVLQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITWLKNGVDVSTQMSKQL 240

QUERY: 363 SLLANGSELHISSVRYEDTGAYTCIAKNEVGVDEDISSLFIEDSARKTLANILWREEGLS 422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 241 SLLANGSELHISSVRYEDTGAYTCIAKNEVGVDEDISSLFIEDSARKTLANILWREEGLS 300

QUERY: 423 VGNMFYVFSDDGIIVIHPVDCEIQRHLKPTEKIFMSYEEICPQREKNATQPCQWVSAVNV 482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 301 VGNMFYVFSDDGIIVIHPVDCEIQRHLKPTEKIFMSYEEICPQREKNATQPCQWVSAVNV 360

QUERY: 483 RNRYIYVAQPALSRVLVVDIQAQKVLQSIGVDPLPAKLSYDKSHDQVWVLSWGDVHKSRP 542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 361 RNRYIYVAQPALSRVLVVDIQAQKVLQSIGVDPLPAKLSYDKSHDQVWVLSWGDVHKSRP 420

QUERY: 543 SLQVITEASTGQSQHLIRTPFAGVDDFFIPPTNLIINHIRFGFIFNKSDPAVHKVDLETM 602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 421 SLQVITEASTGQSQHLIRTPFAGVDDFFIPPTNLIINHIRFGFIFNKSDPAVHKVDLETM 480
```

```
QUERY: 603 MPLKTIGLHHHGCVPQAMAHTHLGGYFFIQCRQDSPASAARQLLVDSVTDSVLGPNGDVT 662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 481 MPLKTIGLHHHGCVPQAMAHTHLGGYFFIQCRQDSPASAARQLLVDSVTDSVLGPNGDVT 540

QUERY: 663 GTPHTSPDGRFIVSAAADSPWLHVQEITVRGEIQTLYDLQINSGISDLAFQRSFTESNQY 722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 541 GTPHTSPDGRFIVSAAADSPWLHVQEITVRGEIQTLYDLQINSGISDLAFQRSFTESNQY 600

QUERY: 723 NIYAALHTEPDLLFLELSTGKVGMLKNLKEPPAGPAQPWGGTHRIMRDSGLFGQYLLTPA 782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 601 NIYAALHTEPDLLFLELSTGKVGMLKNLKEPPAGPAQPWGGTHRIMRDSGLFGQYLLTPA 660

QUERY: 783 RESLFLINGRQNTLRCEVSGIKGGTTVVWVGEV 815
           |||||||||||||||||||||||||||||||||
SBJCT: 661 RESLFLINGRQNTLRCEVSGIKGGTTVVWVGEV 693
```

The amino acid sequence of the FCTR2 protein has 451 of 772 amino acid residues (58%) identical to, and 586 of 772 residues (75%) positive with, the 773 amino acid residue proteins hypothetical protein DKFZp566D234.1 from *Homo sapiens* (fragments) (ptnr: SPTREMBL-ACC: CAB70877.1) (SEQ ID NO:49) (Table 2F).

Table 2F. BLASTP of FCTR2 against hypothetical protein DKFZp566D234.1 (SEQ ID NO:49)

```
>GI|11360192|PIR||T46283 HYPOTHETICAL PROTEIN DKFZP566D234.1 - HUMAN (FRAGMENTS)
 GI|6808053|EMB|CAB70877.1| (AL137695) HYPOTHETICAL PROTEIN [HOMO SAPIENS]
         LENGTH = 773

 SCORE =  911 BITS (2354), EXPECT = 0.0
 IDENTITIES = 451/772 (58%), POSITIVES = 586/772 (75%), GAPS = 7/772 (0%)

QUERY: 49  CVLSRKTGEPECQCLEACRPSYVPVCGSDGRFYENHCKLHRAACLLGKRITVIHSKDCFL 108
           || ||+||+ || |++ |+  | ||||||| |||||++||||||  ++||++|++|||
SBJCT: 2   CVTSRETGQAECACMDLCKRHYKPVCGSDGEFYENHCEVHRAACLKKQKITIVHNEDCFF 61

QUERY: 109 KGDTCTMAGYARLKNVLLALQTRLQPLQEGDSRQ-DPASQKRLLVESLFRDLDADGNGHL 167
           ||| |      +++||+|| || +   +|| ++    |    |+|+|||+ +|+  ||| |  +
SBJCT: 62  KGDKCKTTECSKMKNMLLDLQNQRYIMQENENPNGDDISRKKLLVDQMFKYFDADSNDLV 121

QUERY: 168 SSSELAQHVLKKQDLDEDLLGCSPGDLLRFDDYNSDSSLTLREFYMAFQVVQLSLAPEDR 227
             +|| | |+|+++| +||   |+   ||++||+|+|   | | ||| ||||+||||   + +
SBJCT: 122 DINELTQ-VIKQEELGKDLFDCTLYVLLKYDDFNADKHLALEEFYRAFQVIQLSLPEDQK 180

QUERY: 228 XXXXXXXXXXXXXXXCAVHGDLRPPIIWKRNGLTLNFLDLEDINDFGEDDSLYITKVTTI 287
                          ||+ | |||||||||| + || | ||||||||+| |||||||||
SBJCT: 181 LSITAATVGQSAVLSCAIQGTLRPPIIWKRNNIILNNLGLEDINDFGDDGSLYITKVTTT 240

QUERY: 288 HMGNYTCHASGHEQLFQTHVLQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITW 347
           |+|||||+| |+||++|||+ |||||||||||||||+|||| ||||||||||| |++ |
SBJCT: 241 HVGNYTCYADGYEQVYQTHIFQVNVPPVIRVYPESQAREPGVTASLRCHAEGIPKPQLGW 300

QUERY: 348 LKNGVDVSTQMSKQLSLLANGSELHISSVRYEDTGAYTCIAKNEVGVDEDISSLFIEDSA 407
           ||||+|++ ++||||+| |||||+|||+||||||||||||||| ||||||||||+||||
SBJCT: 301 LKNGIDITPKLSKQLTLQANGSEVHISNVRYEDTGAYTCIAKNEAGVDEDISSLFVEDSA 360

QUERY: 408 RKTLANILWREEGLSVGNMFYVFSDDGIIVIHPVDCEIQRHLKPTEKIFMSYEEICPQRE 467
           ||||||||||||| +||||||| +||| || |++|| |||+||+||+    +|+||   |
SBJCT: 361 RKTLANILWREEGLGIGNMFYVFYEDGIKVIQPIECEFQRHIKPSEKLLGFQDEVCPIAE 420

QUERY: 468 KNATQPCQWVSAVNVRNRYIYVAQPALSRVLVVDIQAQKVLQSIGVDPLPAKLSYDKSHD 527
             +  | | | |||||++++|||||| | |||+||+||+|||+|++  ||+| || ||||||
SBJCT: 421 GDEVQRCVWASAVNVKDKFIYVAQPTLDRVLIVDVQSQKVVQAVSTDPVPVKLHYDKSHD 480
```

```
QUERY: 528 QVWVLSWGDVHKSRPSLQVITEASTGQSQHLIRT-----PFAGVDDFFIPPTNLIINHIR 582
           |||||||| + |+ |+||||| ||       | | |       |  ||||||| | ||| |+|
SBJCT: 481 QVWVLSWGTLEKTSPTLQVITLASGNVPHHTIHTQPVGKQFDRVDDFFIPTTTLIITHMR 540

QUERY: 583 FGFIFNKSDPAVHKVDLETMMPLKTIGLHHHGCVPQAMAHTHLGGYFFIQCRQDSPASAA 642
           |||| +| + |+ |+|||||   +|||  |   + ||||++|+||||||+||  |+ ||   + +
SBJCT: 541 FGFILHKDEAALQKIDLETMSYIKTINLKDYKCVPQSLAYTHLGGYYFIGCKPDSTGAVS 600

QUERY: 643 RQLLVDSVTDSVLGPNGDVTGTPHTSPDGRFIVSAAADSPWLHVQEITVRGEIQTLYDLQ 702
            |++|| |||||+| | ||||||+ |||| ++||          + || ||+|||||   +|+
SBJCT: 601 PQVMVDGVTDSVIGFNSDVTGTPYVSPDGHYLVSINDVKGLVRVQYITIRGEIQEAFDIY 660

QUERY: 703 INSGISDLAFQRSFTESNQYNIYAALHTEPDLLFLELSTGKVGMLKNLKEPPAGPAQPWG 762
             |   ||||||| ||||++||||| +    |+ |+||+|||+|||  |+|+||||        ||
SBJCT: 661 TNLHISDLAFQPSFTEAHQYNIYGSSSTQTDVLFVELSSGKVKMIKSLKEPLKAEEWPWN 720

QUERY: 763 GTHRIMRDSGLFGQYLLTPARESLFLINGRQNTLRCEVSGIKGGTTVVWVGE 814
             +| ++|||||||||+||+++|||+++||  |  |  ||++ ++  |  ||+|||+
SBJCT: 721 RKNRQIQDSGLFGQYLMTPSKDSLFILDGRLNKLNCEITEVEKGNTVIWVGD 772
```

The amino acid sequence of the FCTR2 protein has 61 of 194 amino acid residues (31%) identical to, and 90 of 194 residues (45%) positive with, the 306 amino acid residue protein Follastin-Related Protein 1 Precursor from *Rattus Norvegicus* (ptnr: GenBank Acc:Q62632) (SEQ ID NO:50) (Table 2G).

Table 2G. BLASTP of FCTR2 against Follastatin-Related Protein 1 Precursor from *Rattus Norvegicus* (SEQ ID NO:50)

```
>GI|2498392|SP|Q62632|FRP_RAT FOLLISTATIN-RELATED PROTEIN 1 PRECURSOR
 GI|1083669|PIR||S51361 FOLLISTATIN-RELATED PROTEIN PRECURSOR - RAT
 GI|536900|GB|AAA66063.1| (U06864) FOLLISTATIN-RELATED PROTEIN PRECURSOR [RATTUS
NORVEGICUS]
          LENGTH = 306

 SCORE = 86.4 BITS (213), EXPECT = 1E-15
 IDENTITIES = 61/194 (31%), POSITIVES = 90/194 (45%), GAPS = 26/194 (13%)

QUERY: 38   CGKKFCSRGSRCVLSRKTGEPECQCLEACRPSYVPVCGSDGRFYENHCKLHRAACLLGKR 97
            |   ||  |   | ++ | ||| |  |+| |+|    |||||+|+ |  |||+||| ||| | +
SBJCT: 29   CANVFCGAGRECAVTEK-GEPTCLCIEQCKPHKRPVCGSNGKTYLNHCELHRDACLTGSK 87

QUERY: 98   ITVIHSKDCFLKGD--------TCTMAGYARLKNVLLA-LQTRLQPLQEGDSRQDPASQK 148
            | | +   |  |            |  |      |+  ++  |+  + |       |        |
SBJCT: 88   IQVDYDGHCKEKKSVSPSASPVVCYQANRDELRRRIIQWLEAEIIP----DGWFSKGSNY 143

QUERY: 149  RLLVESLFRDLDADGNGHLSSSELAQHVLK-----------KQDLDEDLLGCSPGDLLRF 197
              +++  |+  | +|+ || |||   + | +                 |+ ++ | |       |+
SBJCT: 144  SEILDKYFKSFD-NGDSHLDSSEFLKFVEQNETAVNITAYPNQENNKLLRGLCVDALIEL 202

QUERY: 198  DDYNSDSSLTLREF 211
             | |+|  |+ +||
SBJCT: 203  SDENADWKLSFQEF 216
```

The amino acid sequence of the FCTR2 protein has 61 of 194 amino acid residues (31%) identical to, and 89 of 194 residues (45%) positive with, the 306 amino acid residue protein Follastin-Related Protein 1 Precursor from *Mus musculus* (GenBank Acc:Q62356) (SEQ ID NO:51) (Table 2H).

Table 2H. BLASTP of FCTR2 against Follastatin-Related Protein 1 Precursor from *Mus musculus* (SEQ ID NO:51)

```
>GI|6679871|REF|NP_032073.1| FOLLISTATIN-LIKE [MUS MUSCULUS]
 GI|2498391|SP|Q62356|FRP_MOUSE FOLLISTATIN-RELATED PROTEIN 1 PRECURSOR (TGF-BETA-
INDUCIBLE PROTEIN
            TSC-36)
 GI|481186|PIR||S38251 FOLLISTATIN-RELATED PROTEIN - MOUSE
 GI|349006|GB|AAC37633.1| (M91380) TGF-BETA-INDUCIBLE PROTEIN [MUS MUSCULUS]
           LENGTH = 306

 SCORE = 85.2 BITS (210), EXPECT = 3E-15
 IDENTITIES = 61/194 (31%), POSITIVES = 89/194 (45%), GAPS = 26/194 (13%)

QUERY: 38   CGKKFCSRGSRCVLSRKTGEPECQCLEACRPSYVPVCGSDGRFYENHCKLHRAACLLGKR 97
            |   ||   |   | ++ | ||| | |+| |+|    |||||+|+ | |||+||| ||| | +
SBJCT: 29   CANVFCGAGRECAVTEK-GEPTCLCIEQCKPHKRPVCGSNGKTYLNHCELHRDACLTGSK 87

QUERY: 98   ITVIHSKDCFLKGDT--------CTMAGYARLKNVLLA-LQTRLQPLQEGDSRQDPASQK 148
            | | +   |  |                | |    |+  |+  |+  + |      |        |
SBJCT: 88   IQVDYDGHCKEKKSASPSASPVVCYQANRDELRRRLIQWLEAEIIP----DGWFSKGSNY 143

QUERY: 149  RLLVESLFRDLDADGNGHLSSSELAQHVLKK-----------QDLDEDLLGCSPGDLLRF 197
              +++  |+  | +|+ || |||   + | +               |+ ++ |          |+
SBJCT: 144  SEILDKYFKSFD-NGDSHLDSSEFLKFVEQNETAINITTYADQENNKLLRSLCVDALIEL 202

QUERY: 198  DDYNSDSSLTLREF 211
             | |+|   |+ +||
SBJCT: 203  SDENADWKLSFQEF 216
```

The amino acid sequence of the FCTR2 protein has 63 of 193 amino acid residues (32%) identical to, and 89 of 193 residues (45%) positive with, the 299 amino acid residue protein Follastatin-Related Protein from the African Clawed Frog (GenBank Acc:JG0187) (SEQ ID NO:52) (Table 2I).

Table 2I. BLASTP of FCTR2 against Follastatin-Related Protein from the African Clawed Frog (SEQ ID NO:52)

```
>GI|7512162|PIR||JG0187 FOLLISTATIN-RELATED PROTEIN - AFRICAN CLAWED FROG
           LENGTH = 299

 SCORE = 81.8 BITS (201), EXPECT = 3E-14
 IDENTITIES = 63/193 (32%), POSITIVES = 89/193 (45%), GAPS = 25/193 (12%)

QUERY: 38   CGKKFCSRGSRCVLSRKTGEPECQCLEACRPSYVPVCGSDGRFYENHCKLHRAACLLGKR 97
            |   ||   |   | ++ | |+| | |+| |+    |||||+|+ | |||+||| ||| | +
SBJCT: 28   CANVFCGAGRECAVTEK-GDPTCDCIEKCKSHKRPVCGSNGKTYLNHCELHRDACLTGSK 86

QUERY: 98   ITVIHSKDCFLK-GDT-------CTMAGYARL-KNVLLALQTRLQPLQEGDSRQDPASQK 148
            | | +   |  |  ||          |  +     + + |+  ||| + |      |        |
SBJCT: 87   IQVDYDGHCKEKTSDTPAAVPVACYQSDRDEMRRRVIHWLQTEITP----DGWFSKGSDY 142

QUERY: 149  RLLVESLFRDLDADGNGHLSSSELAQHVLKKQDL------DED----LLGCSPGDLLRFD 198
              +++  |+  | ||+ || |+||   + + |          ||+     |          |+
SBJCT: 143  SEILDRYFKKFD-DGDSHLDSAELQSFLEQSQSTNITTYKDEETNRMLKSLCVEALIELS 201

QUERY: 199  DYNSDSSLTLREF 211
            | |+|  |    ||
SBJCT: 202  DENADWKLNKNEF 214
```

The amino acid sequence of the FCTR2 protein has 59 of 194 amino acid residues (30%) identical to, and 90 of 194 residues (45%) positive with, the 308 amino acid residue protein Follistatin-Related Protein 1 Precursor from *Homo sapiens* (GenBank Acc:Q12841) (SEQ ID NO:53) (Table 2J).

Table 2J. BLASTP of FCTR2 against Follistatin-Related Protein 1 Precursor from *Homo sapiens* (SEQ ID NO:53)

```
>GI|5901956|REF|NP_009016.1| FOLLISTATIN-LIKE 1 [HOMO SAPIENS]
 GI|2498390|SP|Q12841|FRP_HUMAN FOLLISTATIN-RELATED PROTEIN 1 PRECURSOR
 GI|1082372|PIR||S51362 FOLLISTATIN-RELATED PROTEIN - HUMAN
 GI|536898|GB|AAA66062.1| (U06863) FOLLISTATIN-RELATED PROTEIN PRECURSOR [HOMO
SAPIENS]
 GI|3184393|DBJ|BAA28707.1| (D89937) FOLLISTATIN-RELATED PROTEIN (FRP) [HOMO SAPIENS]
 GI|12652619|GB|AAH00055.1|AAH00055 (BC000055) FOLLISTATIN-LIKE 1 [HOMO SAPIENS]
          LENGTH = 308

 SCORE = 82.9 BITS (204), EXPECT = 1E-14
 IDENTITIES = 59/194 (30%), POSITIVES = 90/194 (45%), GAPS = 26/194 (13%)

QUERY: 38    CGKKFCSRGSRCVLSRKTGEPECQCLEACRPSYVPVCGSDGRFYENHCKLHRAACLLGKR 97
             |   ||  |  | ++ | ||| | |+| |+|   |||||+|+ | |||+||| ||| | +
SBJCT: 31    CANVFCGAGRECAVTEK-GEPTCLCIEQCKPHKRPVCGSNGKTYLNHCELHRDACLTGSK 89

QUERY: 98    ITVIHSKDCFLKGD--------TCTMAGYARLKNVLLA-LQTRLQPLQEGDSRQDPASQK 148
             | | +   |  |           |  +    |+  ++  |+  +  |    |      |
SBJCT: 90    IQVDYDGHCKEKKSVSPSASPVVCYQSNRDELRRRIIQWLEAEIIP----DGWFSKGSNY 145

QUERY: 149   RLLVESLFRDLDADGNGHLSSSELAQHVLKK-----------QDLDEDLLGCSPGDLLRF 197
               +++  |++ | +|+  | |||  + | +            |+ ++ | |     |+
SBJCT: 146   SEILDKYFKNFD-NGDSRLDSSEFLKFVEQNETAINITTYPDQENNKLLRGLCVDALIEL 204

QUERY: 198   DDYNSDSSLTLREF 211
              | |+|  |+ +||
SBJCT: 205   SDENADWKLSFQEF 218
```

The amino acid sequence of the FCTR2 protein has 35 of 69 amino acid residues (50%) identical to, and 45 of 69 residues (64%) positive with, the 315 amino acid residue Flik protein [*Gallus gallus*] (EMBL Acc:CAB42968.1) (SEQ ID NO:54) (Table 2K).

Table 2K. BLASTP of FCTR2 against Flik protein [*Gallus gallus*] (SEQ ID NO:54)

```
>GI|4837645|EMB|CAB42968.1| (AJ238977) FLIK PROTEIN [GALLUS GALLUS]
          LENGTH = 315

 SCORE = 79.8 BITS (196), EXPECT = 1E-13
 IDENTITIES = 35/69 (50%), POSITIVES = 45/69 (64%), GAPS = 1/69 (1%)

QUERY: 38    CGKKFCSRGSRCVLSRKTGEPECQCLEACRPSYVPVCGSDGRFYENHCKLHRAACLLGKR 97
             |   || ||+ | ++ | ||| | |+| |+|   |||||+|+ | |||+||| ||| | +
SBJCT: 31    CANVFCGRGAECAVTEK-GEPTCLCIEQCKPHGRPVCGSNGKTYLNHCELHRDACLTGSK 89

QUERY: 98    ITVIHSKDC 106
             | | +   |
SBJCT: 90    IQVDYDGHC 98
```

The amino acid sequence of the FCTR2 protein has 49 of 152 amino acid residues (32%) identical to, and 65 of 152 residues (42%) positive with a 272-420 amino acid fragment and, 31

of 83 residues (37%) identical to and 44 of 83 residues (52%) positive with a 248-329 amino acid fragment, both of the 1375 amino acid residue Frazzled gene protein [*Drosophila melanogaster*] (GenBankAcc:T13822) (SEQ ID NO:55) (Table 2L).

Table 2L. BLASTP of FCTR2 against Frazzled gene protein [*Drosophila melanogaster*] (SEQ ID NO:55)

```
>GI|7511861|PIR||T13822 FRAZZLED GENE PROTEIN - FRUIT FLY (DROSOPHILA MELANOGASTER)
 GI|1621115|GB|AAC47314.1| (U71001) FRAZZLED [DROSOPHILA MELANOGASTER]
          LENGTH = 1375

 SCORE = 69.4 BITS (169), EXPECT = 2E-10
 IDENTITIES = 49/152 (32%), POSITIVES = 65/152 (42%), GAPS = 4/152 (2%)

QUERY: 243 CAVHGDLRPPIIWKRNGLTLNFLDLEDINDFGEDDSLYITKVTTIHMGNYTCHASGH-EQ 301
           |  +|  +| | | |||+ |+| ||+         || |+    |  ||| | ||    +
SBJCT: 272 CVANGVPKPQIKWLRNGMDLDFNDLDSRFSIVGTGSLQISSAEDIDSGNYQCRASNTVDS 331

QUERY: 302 LFQTHVLQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITWLKNGVDVSTQMSKQ 361
           |      +||  ||     |+            |+|   | | | | |||||  ++     |
SBJCT: 332 LDAQATVQVQEPPKFIKAPKDTTAHEKDEPELKCDIWGKPKPVIRWLKNGDLITPNDYMQ 391

QUERY: 362 LSLLANGSELHISSVRYEDTGAYTCIAKNEVG 393
              | +|  | |  +   | | + |+  |  |
SBJCT: 392 ---LVDGHNLKILGLLNSDAGMFQCVGTNAAG 420

SCORE = 52.9 BITS (126), EXPECT = 1E-05
 IDENTITIES = 31/83 (37%), POSITIVES = 44/83 (52%), GAPS = 2/83 (2%)

QUERY: 311 NVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITWLKNGVDVS-TQMSKQLSLLANGS 369
           +| |   | |  +    |   +| | | |+| |+| ||+||+|+    +  + |++  ||
SBJCT: 248 SVAPSFLVGPSPKTVREGDTVTLDCVANGVPKPQIKWLRNGMDLDFNDLDSRFSIVGTGS 307

QUERY: 370 ELHISSVRYEDTGAYTCIAKNEV 392
            | |||    |+| | | | | |
SBJCT: 308 -LQISSAEDIDSGNYQCRASNTV 329
```

The amino acid sequence of the FCTR2 protein has 53 of 177 amino acid residues (29%) identical to, and 78 of 177 residues (43%) positive with a 366-539 amino acid fragment, 51 of 170 residues (30%) identical to and 74 of 170 residues (43%) positive with a 276-438 amino acid fragment, 46 of 165 amino acid residues (27%) identical to, and 74 of 165 amino acid residues positive with a 185-341 amino acid fragment, 48 of 167 amino acid residues (28%) identical to and 70 of 167 amino acid residues (41%) positive with a 77-243 amino acid fragment, and 28 of 84 amino acid residues (33%) and 37 of 84 amino acid residues positive with a 56-139 amino acid fragment all of the protein 1395 residue Roundabout 1 protein [*Drosophila melanogaster*] (GenBankAcc:AAC38849.1) (SEQ ID NO:56) (Table 2M).

Table 2M. BLASTP of FCTR2 against Roundabout 1 protein [*Drosophila melanogaster*] (SEQ ID NO:56)

```
>GI|2804782|GB|AAC38849.1| (AF040989) ROUNDABOUT 1 [DROSOPHILA MELANOGASTER]
          LENGTH = 1395

 SCORE = 69.8 BITS (170), EXPECT = 1E-10
 IDENTITIES = 53/177 (29%), POSITIVES = 78/177 (43%), GAPS = 11/177 (6%)
```

```
QUERY: 243 CAVHGDLRPPIIWKRNGL-TLNFLDLEDINDF-GEDDSLYITKVTTIHMGNYTCHA---- 296
           |   |+  | +  | +  |+ || |  +       +    | +| || |      | | | |
SBJCT: 366 CMASGNPPPSVFWTKEGVSTLMFPNSSHGRQYVAADGTLQITDVRQEDEGYYVCSAFSVV 425

QUERY: 297 --SGHEQLFQTHVLQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITWLKNGVDV 354
             |      |   +    ||+|++ | +|     |  |+| | | | | ||| |   +|  |
SBJCT: 426 DSSTVRVFLQVSSVDERPPPIIQIGPANQTLPKGSVATLPCRATGNPSPRIKWFHDGHAV 485

QUERY: 355 STQMSKQLSLLANGSELHISSVRYEDTGAYTCIAKNEVGVDEDISSLFIEDSARKTL 411
             |   + |++  || | +  ++  |+| ||| |   | |      ++| +|     +|
SBJCT: 486 --QAGNRYSII-QGSSLRVDDLQLSDSGTYTCTASGERGETSWAATLTVEKPGSTSL 539

SCORE = 56.3 BITS (135), EXPECT = 1E-06
 IDENTITIES = 51/170 (30%), POSITIVES = 74/170 (43%), GAPS = 12/170 (7%)

QUERY: 243 CAVHGDLRPPIIWKRNGLTLNFLDLEDINDFGEDDSLYITKVTTIHMGNYTCHASGH-EQ 301
           |+| ||  | ++||+    +       ++|   + || |+ +|     | | | |   +  |
SBJCT: 276 CSVGGDPPPKVLWKKEEGNIPVSRARILHD---EKSLEISNITPTDEGTYVCEAHNNVGQ 332

QUERY: 302 LFQTHVLQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITWLKNGVDVSTQM--- 358
           +      | |+ ||     | ++          | | | | | | | + | | |  ||| |
SBJCT: 333 ISARASLIVHAPPNFTKRPSNKKVGLNGVVQLPCMASGNPPPSVFWTKEG--VSTLMFPN 390

QUERY: 359 -SKQLSLLANGSELHISSVRYEDTGAYTCIAKNEVGVDEDISSLFIEDSA 407
            |     +|    | |+ || || | | | | +    ||     +|++ |+
SBJCT: 391 SSHGRQYVAADGTLQITDVRQEDEGYYVCSAFSV--VDSSTVRVFLQVSS 438

SCORE = 51.7 BITS (123), EXPECT = 3E-05
 IDENTITIES = 46/165 (27%), POSITIVES = 74/165 (43%), GAPS = 20/165 (12%)

QUERY: 251 PPIIWKRNGLTLNFLDLEDINDFG--------EDDSLYITKVTTIHMGNYTCHASG---- 298
           | +|| ++|+ |+  ||+ ++ ||          +  +| |+ |   |   ||| | |
SBJCT: 185 PTLIWIKDGVPLD--DLKAMS-FGASSRVRIVDGGNLLISNVEPIDEGNYKCIAQNLVGT 241

QUERY: 299 HEQLFQTHVLQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITWLKNGVDVSTQM 358
             | +   ++||   |    |+ |    |  |+  |    | | |++ | |    ++
SBJCT: 242 RESSYAKLIVQVK--PYFMKEPKDQVMLYGQTATFHCSVGGDPPPKVLWKKEEGNIPVSR 299

QUERY: 359 SKQLSLLANGSELHISSVRYEDTGAYTCIAKNEVGVDEDISSLFI 403
           ++   +| +   | ||++  | | | | | | | ||     +|| +
SBJCT: 300 AR---ILHDEKSLEISNITPTDEGTYVCEAHNNVGQISARASLIV 341

SCORE = 44.0 BITS (103), EXPECT = 0.007
 IDENTITIES = 48/167 (28%), POSITIVES = 70/167 (41%), GAPS = 13/167 (7%)

QUERY: 243 CAVHGDLRPPIIWKRNGLTLNFLDLEDINDFGEDDSLYITKVTTIHM----GNYTCHASG 298
           | | |   | | | ++|  ++  + +     +| +|+  +             | | | |
SBJCT: 77  CKVEGKPEPTIEWFKDGEPVSTNEKKSHRVQFKDGALFFYRTMQGKKEQDGGEYWCVAKN 136

QUERY: 299 H-EQLFQTHV-LQVNV-PPVIRVYPESQAQEPGVAASLRCH-AEGIPMPRITWLKNGVDV 354
             |    |  ||+ |      || |+      | | | |    +||| | + |+|+|| +
SBJCT: 137 RVGQAVSRHASLQIAVLRDDFRVEPKDTRVAKGETALLECGPPKGIPEPTLIWIKDGVPL 196

QUERY: 355 STQMSKQLSL-----LANGSELHISSVRYEDTGAYTCIAKNEVGVDE 396
              +          + +|  | ||+|  | | | |||+| ||  |
SBJCT: 197 DDLKAMSFGASSRVRIVDGGNLLISNVEPIDEGNYKCIAQNLVGTRE 243

SCORE = 42.9 BITS (100), EXPECT = 0.014
 IDENTITIES = 28/84 (33%), POSITIVES = 37/84 (43%), GAPS = 4/84 (4%)

QUERY: 314 PVIRVYPESQAQEPGVAASLRCHAEGIPMPRITWLKNGVDVSTQMSKQLSLLANGSELH- 372
           | |  +|      +    |+| |  || | | | | |+|  |||   |   +       |
SBJCT: 56  PRIIEHPTDLVVKKNEPATLNCKVEGKPEPTIEWFKDGEPVSTNEKKSHRVQFKDGALFF 115

QUERY: 373 ---ISSVRYEDTGAYTCIAKNEVG 393
              +   + +| | | |+||| ||
SBJCT: 116 YRTMQGKKEQDGGEYWCVAKNRVG 139
```

The amino acid sequence of the FCTR2 protein has 55 of 157 amino acid residues (35%) identical to, and 75 of 157 residues (47%) positive with a 620-775 amino acid fragment, 49 of 163 residues (30%) identical to and 71 of 163 residues (43%) positive with a 335-492 amino acid fragment, 32 of 85 amino acid residues (37%) identical to, and 48 of 85 amino acid residues (55%) positive with a 1305-1388 amino acid fragment, 37 of 143 amino acid residues (25%) identical to and 60 of 143 amino acid residues (41%) positive with a 183-319 amino acid fragment, 43 of 174 amino acid residues (24%) and 70 of 174 amino acid residues (39%) positive with a 711-884 amino acid fragment, and 46 of 165 residues (27%) identical to and 69 of 165 residues positive with a 831-884 amino acid fragment all of the protein 1395 residue Down Syndrome Cell Adhesion Molecule Precursor (CHD2) from *Homo Sapiens* (GenBankAcc:O60469) (SEQ ID NO:57) (Table 2N).

Table 2N. BLASTP of FCTR2 against Down Syndrome Cell Adhesion Molecule Precursor (SEQ ID NO:57)

```
>gi|12643619|sp|O60469|DSCA_HUMAN DOWN SYNDROME CELL ADHESION MOLECULE PRECURSOR
(CHD2)
 GI|6740013|GB|AAF27525.1|AF217525_1 (AF217525) DOWN SYNDROME CELL ADHESION MOLECULE
[HOMO SAPIENS]
          LENGTH = 2012

 SCORE = 70.6 BITS (172), EXPECT = 6E-11
 IDENTITIES = 55/157 (35%), POSITIVES = 75/157 (47%), GAPS = 7/157 (4%)

QUERY: 245 VHGDLRPPIIWKRNGLTLNFLDLEDINDFGEDDSLYITKVTTIHMGNYTCHASGHEQLFQ 304
            | |||   | |+++|  +       |++      || |+ ++ +| ||||| |       +
SBJCT: 620 VSGDLPITITWQKDGRPIPGSLGVTIDNIDFTSSLRISNLSLMHNGNYTCIARNEAAAVE 679

QUERY: 305 THV-LQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITW-LKNGVDVST----QM 358
               | | |||  | |  |      | |  | | ||| |+| | |     | |      +
SBJCT: 680 HQSQLIVRVPPKFVVQPRDQDGIYGKAVILNCSAEGYPVPTIVWKFSKGAGVPQFQPIAL 739

QUERY: 359 SKQLSLLANGSELHISSVRYEDTGAYTCIAKNEVGVD 395
           + ++ +|+||| | |  |  ||+| | |  |+|| |
SBJCT: 740 NGRIQVLSNGS-LLIKHVVEEDSGYYLCKVSNDVGAD 775

SCORE = 50.6 BITS (120), EXPECT = 7E-05
 IDENTITIES = 49/163 (30%), POSITIVES = 71/163 (43%), GAPS = 16/163 (9%)

QUERY: 243 CAVHGDLRPPIIWKRNGLTLNFLDLEDINDFGEDDSLYITKVTTIHMGNYTCHASGHEQL 302
           |+| |     + | ||| ||        |      ++ | +  +     | | |      +
SBJCT: 335 CSVTGTEDQELSWYRNGEILNPGKNVRITGINHEN-LIMDHMVKSDGGAYQCFVRKDKLS 393

QUERY: 303 FQTH---VLQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITW-------LKNGV 352
             | +   ||+   | +|  + | +   |     || |+ +| |+| |||       || |
SBJCT: 394 AQDYVQVVLEDGTPKIISAFSE-KVVSPAEPVSLMCNVKGTPLPTIITWTLDDDPILKGG- 451

QUERY: 353 DVSTQMSKQLSLLAN-GSELHISSVRYEDTGAYTCIAKNEVGV 394
             | ++|+ ++   |  | |+||| +  | | | | | |  ||
SBJCT: 452 --SHRISQMITSEGNVVSYLNISSSQVRDGGVYRCTANNSAGV 492

SCORE = 47.9 BITS (113), EXPECT = 5E-04
 IDENTITIES = 32/85 (37%), POSITIVES = 48/85 (55%), GAPS = 6/85 (7%)

QUERY: 333  LRCHAEGIPMPRITWLK--NGVDVSTQMSKQLSLLANGSELHISSVRYEDTGAYTCIAKN 390
            | | | | | | | + |+|  ||        +  + |+ +||| + | +|+ ||+| |+||| |
SBJCT: 1305 LPCKAVGDPSPAVKWMKDSNGTPSLVTIDGRRSIFSNGSFI-IRTVKAEDSGYYSCIANN 1363
```

```
QUERY: 391  EVGVDEDISSLFIE---DSARKTLA 412
              | || | +| ++   |  | |++
SBJCT: 1364 NWGSDEIILNLQVQVPPDQPRLTVS 1388

SCORE = 42.9 BITS (100), EXPECT = 0.015
 IDENTITIES = 37/143 (25%), POSITIVES = 60/143 (41%), GAPS = 6/143 (4%)

QUERY: 270 INDFGEDDSLYITKVTTIHMGNYTCHASGHEQLFQTHVLQVNVPPVIRVYPESQAQEPGV 329
           | |   +| || +  | |        |   +|| +     |  | |    + +    |
SBJCT: 183 IKDVQNEDGLYNYRCITRHRYTGETRQSNSARLFVSD--PANSAPSILDGFDHRKAMAGQ 240

QUERY: 330 AASLRCHAEGIPMPRITWLKNGVDVSTQMSKQLSLLANGSELHISSVRYEDTGAYTCIAK 389
              | | | | | |   |||+  ++  ++| +      |  | | ++|  |+|+| |
SBJCT: 241 RVELPCKALGHPEPDYRWLKD--NMPLELSGRFQKTVTG--LLIENIRPSDSGSYVCEVS 296

QUERY: 390 NEVGVDEDISSLFIEDSARKTLA 412
           |  |  + |  |+++   + |++
SBJCT: 297 NRYGTAKVIGRLYVKQPLKATIS 319

 SCORE = 41.3 BITS (96), EXPECT = 0.047
 IDENTITIES = 43/174 (24%), POSITIVES = 70/174 (39%), GAPS = 11/174 (6%)

QUERY: 243 CAVHGDLRPPIIWK--RNGLTLNF--LDLEDINDFGEDDSLYITKVTTIHMGNYTCHASG 298
           |+  |   | |+||  +      |  + |        + || |  |     | | |  |
SBJCT: 711 CSAEGYPVPTIVWKFSKGAGVPQFQPIALNGRIQVLSNGSLLIKHVVEEDSGYYLCKVSN 770

QUERY: 299 H--EQLFQTHVLQVNVPPVIRVYPESQAQEPGVAASLRCHAEGIPMPRITWLKNGVDVST 356
                + ++  | | +| +|  || +     |    + | | |     + | |    ++
SBJCT: 771 DVGADVSKSMYLTVKIPAMITSYPNTTLATQGQKKEMSCTAHGEKPIIVRWEKEDRIINP 830

QUERY: 357 QMSKQLSLLANGSELHISSVRY-----EDTGAYTCIAKNEVGVDEDISSLFIED 405
           +|++ |       |  ||+++      ||+| ++| | |  | |  |  | +++
SBJCT: 831 EMARYLVSTKEVGEEVISTLQILPTVREDSGFFSCHAINSYGEDRGIIQLTVQE 884

SCORE = 40.6 BITS (94), EXPECT = 0.074
 IDENTITIES = 46/165 (27%), POSITIVES = 69/165 (40%), GAPS = 7/165 (4%)

QUERY: 243 CAVHGDLRPPIIWKRNGLTLNFLDLEDINDFGEDDSLYITKVTT-IHMGNYTCHASGHEQ 301
           | | |     | | +|   | |   +    |  + +| ++ |   +  | |||+     |
SBJCT: 525 CRVIGYPYYSIKWYKNSNLLPFNHRQVA--FENNGTLKLSDVQKEVDEGEYTCNVLVQPQ 582

QUERY: 302 LFQTHVLQVN--VPPVIRVYPESQAQEPGVAASLRCHAEGIPMP-RITWLKNGVDVSTQM 358
           |  +  + |   ||| |+ + |      |    + |      +|  ||| |+|  +   +
SBJCT: 583 LSTSQSVHVTVKVPPFIQPF-EFPRFSIGQRVFIPCVVVSGDLPITITWQKDGRPIPGSL 641

QUERY: 359 SKQLSLLANGSELHISSVRYEDTGAYTCIAKNEVGVDEDISSLFI 403
              +  +   | | ||++     | |||||+||    |  |  | +
SBJCT: 642 GVTIDNIDFTSSLRISNLSLMHNGNYTCIARNEAAAVEHQSQLIV 686
```

The amino acid sequence of the FCTR2 protein has 55 of 194 amino acid residues (28%) identical to, and 86 of 194 residues (44%) positive with Limbic System-Associated Membrane Protein Precursor (LSAMP) from *Homo sapiens* (SWISSPROT Acc:Q13449) (SEQ ID NO:58) (Table 2O).

Table 2O. BLASTP of FCTR2 against Limbic System-Associated Membrane Protein Precursor (SEQ ID NO:58)

```
PTNR:SWISSPROT-ACC:Q13449 LIMBIC SYSTEM-ASSOCIATED MEMBRANE PROTEIN PRECURSOR
(LSAMP) - HOMO SAPIENS (HUMAN), 338 AA.

          LENGTH = 338

 SCORE = 191 (67.2 BITS), EXPECT = 6.7E-12, P = 6.7E-12
 IDENTITIES = 55/194 (28%), POSITIVES = 86/194 (44%)
```

The amino acid sequence of the FCTR2 protein has 68 of 190 amino acid residues (35%) identical to, and 92 of 190 residues (48%) positive with Putative Neuronal Cell Adhesion Molecule, Short Form from *Mus musculus* (SPTREMBL Acc:O70246) (SEQ ID NO:59) (Table 2P).

Table 2P. BLASTP of FCTR2 against Putative Neuronal Cell Adhesion Molecule, Short Form from *Mus musculus* (SEQ ID NO:59)

```
PTNR:SPTREMBL-ACC:O70246 PUTATIVE NEURONAL CELL ADHESION MOLECULE (PUNC)
(PUTATIVE NEURONAL CELL ADHESION MOLECULE, SHORT FORM) - MUS MUSCULUS
(MOUSE), 793 AA
          LENGTH = 793

 SCORE = 203 (71.5 BITS), EXPECT = 7.0E-12, SUM P(2) = 7.0E-12
 IDENTITIES = 68/190 (35%), POSITIVES = 92/190 (48%)
```

The amino acid sequence of the FCTR2 protein has 58 of 199 amino acid residues (29%) identical to, and 91 of 199 residues (45%) positive with CHLAMP, G11-Isoform Precursor from *Gallus gallus* (SPTREMBL Acc: O02869) (SEQ ID NO:60) (Table 2Q).

Table 2Q. BLASTP of FCTR2 against CHLAMP, G11-Isoform Precursor from *Gallus gallus* (SEQ ID NO:60)

```
PTNR:SPTREMBL-ACC:O02869 CHLAMP, G11-ISOFORM PRECURSOR - GALLUS GALLUS
(CHICKEN), 350 AA.
          LENGTH = 350

 SCORE = 191 (67.2 BITS), EXPECT = 7.7E-12, P = 7.7E-12
 IDENTITIES = 58/199 (29%), POSITIVES = 91/199 (45%)
```

The amino acid sequence of the FCTR2 protein has 55 of 194 amino acid residues (28%) identical to, and 86 of 194 residues (44%) positive with Limbic System-Associated Membrane Protein Precursor (LSAMP) from *Rattus norvegicus* (SWISSPROT Acc:Q62813) (SEQ ID NO:61) (Table 2R).

Table 2R. BLASTP of FCTR2 against Limbic System-Associated Membrane Protein Precursor (LSAMP) from *Rattus norvegicus* (SEQ ID NO:61)

```
PTNR:SWISSPROT-ACC:Q62813 LIMBIC SYSTEM-ASSOCIATED MEMBRANE PROTEIN PRECURSOR
(LSAMP) - RATTUS NORVEGICUS (RAT), 338 AA.
          LENGTH = 338

 SCORE = 188 (66.2 BITS), EXPECT = 1.5E-11, P = 1.5E-11
 IDENTITIES = 55/194 (28%), POSITIVES = 86/194 (44%)
```

FCTR2 protein has similarity to cell adhesion molecules, follistatin, roundabout and frazzled (see BlastP results). These genes are involved in neuronal development and

reproductive physiology. Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is required for CNS and motor axon guidance (Cell 87:197-204(1996)). Characterization of a rat C6 glioma-secreted follistatin-related protein (FRP) and cloning and sequence of the human homologue is described in Eur. J. Biochem. 225:937-946(1994). This protein may modulate the action of some growth factors on cell proliferation and differentiation. FRP binds heparin. The follistatin-related protein is a secreted protein and has one follistatin-like domain. The cloning and early dorsal axial expression of Flik, a chick follistatin-related gene and evidence for involvement in dorsalization/neural induction is presented in Dev. Biol. 178:327-342(1996). Roundabout controls axon crossing of the CNS midline and defines a novel subfamily of evolutionarily conserved guidance receptors, as shown in Cell 92:205-215(1998). cDNA cloning and structural analysis of the human limbic-system- associated membrane protein (LAMP) is described in Gene 170:189-195(1996). LAMP, a protein of the OBCAM family that contains three immunoglobulin-like C2-type domains, mediates selective neuronal growth and axon targeting. LAMP contributes to the guidance of developing axons and remodeling of mature circuits in the limbic system. This protein is essential for normal growth of the hippocampal mossy fiber projection. LAMP is attached to the membrane by a GPI-Anchor. It is expressed on limbic neurons and fiber tracts as well as in single layers of the superior colliculus, spinal chord and cerbellum. Characterization of the human full-length PTK7 cDNA encoding a receptor protein tyrosine kinase-like molecule closely related to chick KLG is disclosed in J. Biochem. 119:235-239(1996). Based upon homology, FCTR2 proteins and each homologous protein or peptide may share at least some activity.

Functions and therapeutic uses:

The OMIM gene map has identified this region which the invention maps to (5q21-5q31) as associated with susceptibility to the following diseases (OMIM Ids are underlined):

- Allergy and asthma
- Hemangioma,
- capillary infantile Schistosoma mansoni infection, susceptibility/resistance to Spinocerebellar ataxia
- Bronchial asthma
- Plasmodium falciparum parasitemia,
- intensity of Corneal dystrophy, Groenouw type I, <u>121900</u>; Corneal dystrophy,lattice type I, <u>122200</u>;
- Reis-Bucklers corneal dystrophy;Corneal dystrophy, Avellino type Eosinophilia, familial Myelodysplastic syndrome;

- Myelogenous leukemia, Acute Cutis laxa, recessive, type I, Deafness, autosomal dominant nonsyndromic sensorineural, 1 Contractural arachnodactyly, Congenital Neonatal alloimmune thrombocytopenia;
- Glycoprotein Ia deficiency Male infertility;
- Charcot-Marie-Tooth neuropathy, Demyelinating Gardner syndrome ;
- Adenomatous polyposis coli;
- Colorectal cancer;
- Desmoid disease, hereditary, <u>135290</u>;
- Turcot syndrome,<u>276300</u>;
- Adenomatous polyposis coli, attenuated
- Colorectal cancer

Therefore the invention is implicated in at least all of the above mentioned diseases and may have therapeutic uses for these diseases.

This sequence has similarity to cell adhesion molecules, follistatin, roundabout and frazzled (see BlastP results). These genes are involved in neuronal development and reproductive physiology. Therefore the invention is also implicated in disorders such as or therapeutic uses for:

- Neurodegenerative disorders, nerve trauma, epilepsy, mental health conditions
- Tissue regeneration in vivo and in vitro

Female reproductive system disorders and pregnancy

FCTR3

FCTR3, is an amino acid type II membrane, neurestin-like protein. The FCTR3a nucleic acid of 1430 nucleotides (also designated 10129612.0.118) is shown in Table 3A. An ORF was identified beginning with an ATG initiation codon at nucleotides 69-71 and ending with a TAG codon at nucleotides 1212-1214. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 3A, and the start and stop codons are in bold letters.

Table 3A. FCTR3a Nucleotide Sequence (SEQ ID NO:5)

<u>AAAAAAGGCGGGGGGTGGACTTAGCAGTGTAATTTGAGACCGGTGGTAAGGATTGGAGCGAGCTAGAG</u>**ATG**CTGCACGCTGCTAACA
AGGGAAGGAAGCCTTCAGCTGAGGCAGGTCGTCCCATTCCACCTACATCCTCGCCTAGTCTCCTCCCATCTGCTCAGCTGCCTAGCT
CCCATAATCCTCCACCAGTTAGCTGCCAGATGCCATTGCTAGACAGCAACACCTCCCATCAAATCATGGACACCAACCCTGATGAGG
AATTCTCCCCCAATTCATACCTGCTCAGAGCATGCTCAGGGCCCCAGCAAGCCTCCAGCAGTGGCCCTCCGAACCACCACAGCCAGT
CGACTCTGAGGCCCCCTCTCCCACCCCCTCACAACCACACGCTGTCCCATCACCACTCGTCCGCCAACTCCCTCAACAGGAACTCAC
TGACCAATCGGCGGAGTCAGATCCACGCCCCGGCCCCAGCGCCCAATGACCTGGCCACCACACCAGAGTCCGTTCAGCTTCAGGACA
GCTGGGTGCTAAACAGCAACGTGCCACTGGAGACCCGGCACTTCCTCTTCAAGACCTCCTCGGGGAGCACACCCTTGTTCAGCAGCT

CTTCCCCGGGATACCCTTTGACCTCAGGAACGGTTTACACGCCCCCGCCCCGCCTGCTGCCCAGGAATACTTTCTCCAGGAAGGCTT
TCAAGCTGAAGAAGCCCTCCAAATACTGCAGCTGGAAATGTGCTGCCCTCTCCGCCATTGCCGCGGCCCTCCTCTTGGCTATTTTGC
TGGCGTATTTCATAGTGCCCTGGTCGTTGAAAAACAGCAGCATAGACAGTGGTGAAGCAGAAGTTGGTCGGCGGGTAACACAAGAAG
TCCCACCAGGGGTGTTTTGGAGGTCACAAATTCACATCAGTCAGCCCCAGTTCTTAAAGTTCAACATCTCCCTCGGGAAGGACGCTC
TCTTTGGTGTTTACATAAGAAGAGGACTTCCACCATCTCATGCCCAGTATGACTTCATGGAACGTCTGGACGGGAAGGAGAAGTGGA
GTGTGGTTGAGTCTCCCAGGGAACGCCGGAGCATACAGACCTTGGTTCAGAATGAAGCCGTGTTTGTGCAGTACCTGGATGTGGGCC
TGTGGCATCTGGCCTTCTACAATGATGGAAAAGACAAAGAGATGGTTTCCTTCAATACTGTTGTCCTAGATGGGACCATC**TAG**TTGC
AGAAAAACAAGCTCAGGGCGCCCACTGATTTGACATTATGATTCAGTGCAGGACTGTCCACGTAACTGCCATGGAATGGTGAATGT
GTGTCCGGGGTGTGTCACTGTTTCCCAGGATTTCTAGGAGCAGACTGTGCTAAAGACCTTCCTGCCTTGACTTTCTGCAAGACAATC
ATTAATAAAGCTGCTCTGTAAATACTAAAAAAAAAACA

The FCTR3 polypeptide (SEQ ID NO:5) encoded by SEQ ID NO:5 is 381 amino acid residues and is presented using the one-letter code in Table 3B.

Table 3B. Encoded FCTR3a protein sequence (SEQ ID NO:6).

MLHAANKGRKPSAEAGRPIPPTSSPSLLPSAQLPSSHNPPPVSCQMPLLDSNTSHQIMDTNPDEEFSPNSYLLRACSGPQQASSSGP
PNHHSQSTLRPPLPPPHNHTLSHHHSSANSLNRNSLTNRRSQIHAPAPAPNDLATTPESVQLQDSWVLNSNVPLETRHFLFKTSSGS
TPLFSSSSPGYPLTSGTVYTPPPRLLPRNTFSRKAFKLKKPSKYCSWKCAALSAIAAALLLAILLAYFIVPWSLKNSSIDSGEAEVG
RRVTQEVPPGVFWRSQIHISQPQFLKFNISLGKDALFGVYIRRGLPPSHAQYDFMERLDGKEKWSVVESPRERRSIQTLVQNEAVFV
QYLDVGLWHLAFYNDGKDKEMVSFNTVVLDGTI

In an alternative embodiment, the 5' end of the FCTR3a nucleic acid could be extended as it is in the 9826bp FCTR3b (also referred to herein as 10129612.0.405) shown in Table 3C. An ORF was identified beginning with an ATG initiation codon at nucleotides 280-282 and ending with a TAA codon at nucleotides 8479-8481. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 3C, and the start and stop codons are in bold letters. Italicized bases 1-201 refer to a variable 5' region that will be further discussed below.

Table 3C. FCTR3b Nucleotide Sequence (SEQ ID NO:7)

TTTAAATCCTCATACCTTAAAGGAGATGTGTATATAAGGGAGTTGGAACCAGCATTAGATGAGTTGACAAAAATGCAGTT
TCAGTTCTAGAGGTCTGGGAAGTCCAAGAACAAGGTGCTGGCAGATTGGATTCCCCGTGAGGGCTTTCTTCCTGGCTTGA
*AGTTGGCTGCTTTCCTGCTGAGACTTCTCATGGCAGAGACT*GAGGGTGGCAAAGTGACAAGTGCCAAAACTCAGGCCTGA
CTTTTCTGAAAACATCAGCATTCTGCCATATCTGGAATA**ATG**GATGTAAAGGACCGGCGACACCGCTCTTTGACCAGAGG
ACGCTGTGGCAAAGAGTGTCGCTACACAAGCTCCTCTCTGGACAGTGAGGACTGCCGGGTGCCCACACAGAAATCCTACA
GCTCCAGTGAGACTCTGAAGGCCTATGACCATGACAGCAGGATGCACTATGGAAACCGAGTCACAGACCTCATCCACCGG
GAGTCAGATGAGTTTCCTAGACAAGGAACCAACTTCACCCTTGCCGAACTGGGCATCTGTGAGCCCTCCCCACACCGAAG
CGGCTACTGCTCCGACATGGGGATCCTTCACCAGGGCTACTCCCTTAGCACAGGGTCTGACGCCGACTCCGACACCGAGG
GAGGGATGTCTCCAGAACACGCCATCAGACTGTGGGGCAGAGGGATAAAATCCAGGCGCAGTTCCGGCCTGTCCAGTCGT
GAAAACTCGGCCCTTACCCTGACTGACTCTGACAACGAAAACAAATCAGATGATGAGAACGGTCGTCCCATTCCACCTAC
ATCCTCGCCTAGTCTCCTCCCATCTGCTCAGCTGCCTAGCTCCCATAATCCTCCACCAGTTAGCTGCCAGATGCCATTGC
TAGACAGCAACACCTCCCATCAAATCATGGACACCAACCCTGATGAGGAATTCTCCCCCAATTCATACCTGCTCAGAGCA
TGCTCAGGGCCCCAGCAAGCCTCCAGCAGTGGCCCTCCGAACCACCACAGCCAGTCGACTCTGAGGCCCCCTCTCCCACC
CCCTCACAACCACACGCTGTCCCATCACCACTCGTCCGCCAACTCCCTCAACAGGAACTCACTGACCAATCGGCGGAGTC
AGATCCACGCCCCGGCCCCAGCGCCCAATGACCTGGCCACCACACCAGAGTCCGTTCAGCTTCAGGACAGCTGGGTGCTA
AACAGCAACGTGCCACTGGAGACCCGGCACTTCCTCTTCAAGACCTCCTCGGGGAGCACACCCTTGTTCAGCAGCTCTTC
CCCGGGATACCCTTTGACCTCAGGAACGGTTTACACGCCCCCGCCCCGCCTGCTGCCCAGGAATACTTTCTCCAGGAAGG
CTTTCAAGCTGAAGAAGCCCTCCAAATACTGCAGCTGGAAATGTGCTGCCCTCTCCGCCATTGCCGCGGCCCTCCTCTTG
GCTATTTTGCTGGCGTATTTCATAGTGCCCTGGTCGTTGAAAAACAGCAGCATAGACAGTGGTGAAGCAGAAGTTGGTCG
GCGGGTAACACAAGAAGTCCCACCAGGGGTGTTTTGGAGGTCACAAATTCACATCAGTCAGCCCCAGTTCTTAAAGTTCA
ACATCTCCCTCGGGAAGGACGCTCTCTTTGGTGTTTACATAAGAAGAGGACTTCCACCATCTCATGCCCAGTATGACTTC
ATGGAACGTCTGGACGGGAAGGAGAAGTGGAGTGTGGTTGAGTCTCCCAGGGAACGCCGGAGCATACAGACCTTGGTTCA
GAATGAAGCCGTGTTTGTGCAGTACCTGGATGTGGGCCTGTGGCATCTGGCCTTCTACAATGATGGAAAAGACAAAGAGA
TGGTTTCCTTCAATACTGTTGTCCTAGATTCAGTGCAGGACTGTCCACGTAACTGCCATGGAATGGTGAATGTGTGTCC
GGGGTGTGTCACTGTTTCCCAGGATTTCTAGGAGCAGACTGTGCTAAAGCTGCCTGCCCTGTCCTGTGCAGTGGGAATGG
ACAATATTCTAAAGGACGTGCCAGTGCTACAGCGGCTGGAAAGGTGCAGAGTGCGACGTGCCCATGAATCAGTGCATCG
ATCCTTCCTGCGGGGGCCACGGCTCCTGCATTGATGGGAACTGTGTCTGCTCTGCTGGCTACAAAGGCGAGCACTGTGAG

GAAGTTGATTGCTTGGATCCCACCTGCTCCAGCCACGGAGTCTGTGTGAATGGAGAATGCCTGTGCAGCCCTGGCTGGGG
TGGTCTGAACTGTGAGCTGGCGAGGGTCCAGTGCCCAGACCAGTGCAGTGGGCATGGCACGTACCTGCCTGACACGGGCC
TCTGCAGCTGCGATCCCAACTGGATGGGTCCCGACTGCTCTGTTGAAGTGTGCTCAGTAGACTGTGGCACTCACGGCGTC
TGCATCGGGGGAGCCTGCCGCTGTGAAGAGGGCTGGACAGGCGCAGCGTGTGACCAGCGCGTGTGCCACCCCCGCTGCAT
TGAGCACGGGACCTGTAAAGATGGCAAATGTGAATGCCGAGAGGGCTGGAATGGTGAACACTGCACCATTGGTAGGCAAA
CGGCAGGCACCGAAACAGATGGCTGCCCTGACTTGTGCAACGGTAACGGGAGATGCACACTGGGTCAGAACAGCTGGCAG
TGTGTCTGCCAGACCGGCTGGAGAGGGCCCGGATGCAACGTTGCCATGGAAACTTCCTGTGCTGATAACAAGGATAATGA
GGGAGATGGCCTGGTGGATTGTTTGGACCCTGACTGCTGCCTGCAGTCAGCCTGTCAGAACAGCCTGCTCTGCCGGGGGT
CCCGGGACCCACTGGACATCATTCAGCAGGGCCAGACGGATTGGCCCGCAGTGAAGTCCTTCTATGACCGTATCAAGCTC
TTGGCAGGCAAGGATAGCACCCACATCATTCCTGGAGAGAACCCTTTCAACAGCAGCTTGGTTTCTCTCATCCGAGGCCA
AGTAGTAACTACAGATGGAACTCCCCTGGTCGGTGTGAACGTGTCTTTTGTCAAGTACCCAAAATACGGCTACACCATCA
CCCGCCAGGATGGCACGTTCGACCTGATCGCAAATGGAGGTGCTTCCTTGACTCTACACTTTGAGCGAGCCCCGTTCATG
AGCCAGGAGCGCACTGTGTGGCTGCCGTGGAACAGCTTTTACGCCATGGACACCCTGGTGATGAAGACCGAGGAGAACTC
CATCCCCAGCTGTGACCTCAGTGGCTTTGTCCGGCCTGATCCAATCATCATCTCCTCCCCACTGTCCACCTTCTTTAGTG
CTGCCCCTGGGCAGAATCCCATCGTGCCTGAGACCCAGGTTCTTCATGAAGAAATCGAGCTCCCTGGTTCCAATGTGAAA
CTTCGCTATCTGAGCTCTAGAACTGCAGGGTACAAGTCACTGCTGAAGATCACCATGACCCAGTCCACAGTGCCCCTGAA
CCTCATTAGGGTTCACCTGATGGTGGCTGTCGAGGGGCATCTCTTCCAGAAGTCATTCCAGGCTTCTCCCAACCTGGCCT
CCACCTTCATCTGGGACAAGACAGATGCGTATGGCCAAAGGGTGTATGGACTCTCAGATGCTGTTGTGTCTGTCGGGTTT
GAATATGAGACCTGTCCCAGTCTAATTCTCTGGGAGAAAAGGACAGCCCTCCTTCAGGGATTCGAGCTGGACCCCTCCAA
CCTCGGTGGCTGGTCCCTAGACAAACACCACATCCTCAATGTTAAAAGTGGAATCCTACACAAAGGCACTGGGAAAACC
AGTTCCTGACCCAGCAGCCTGCCATCATCACCAGCATCATGGGCAATGGTCGCCGCCGGAGCATTTCCTGTCCCAGCTGC
AACGGCCTTGCTGAAGGCAACAAGCTGCTGGCCCCAGTGGCTCTGGCTGTTGGAATCGATGGGAGCCTCTATGTGGGTGA
CTTCAATTACATCCGACGCATCTTTCCCTCTCGAAATGTGACCAGCATCTTGGAGTTACGAAATAAAGAGTTTAAACATA
GCAACAACCCAGCACACAAGTACTACTTGGCAGTGGACCCCGTGTCCGGCTCGCTCTACGTGTCCGACACCAACAGCAGG
AGAATCTACCGCGTCAAGTCTCTGAGTGGAACCAAAGACCTGGCTGGGAATTCGGAAGTTGTGGCAGGGACGGGAGAGCA
GTGTCTACCCTTTGATGAAGCCCGCTGCGGGGATGGAGGGAAGGCCATAGATGCAACCCTGATGAGCCCGAGAGGTATTG
CAGTAGACAAGAATGGGCTCATGTACTTTGTCGATGCCACCATGATCCGGAAGGTTGACCAGAATGGAATCATCTCCACC
CTGCTGGGCTCCAATGACCTCACTGCCGTCCGGCCGCTGAGCTGTGATTCCAGCATGGATGTAGCCCAGGTTCGTCTGGA
GTGGCCAACAGACCTTGCTGTCAATCCCATGGATAACTCCTTGTATGTTCTAGAGAACAATGTCATCCTTCGAATCACCG
AGAACCACCAAGTCAGCATCATTGCGGGACGCCCCATGCACTGCCAAGTTCCTGGCATTGACTACTCACTCAGCAAACTA
GCCATTCACTCTGCCCTGGAGTCAGCCAGTGCCATTGCCATTTCTCACACTGGGGTCCTCTACATCACTGAGACAGATGA
GAAGAAGATTAACCGTCTACGCCAGGTAACAACCAACGGGGAGATCTGCCTTTTAGCTGGGGCAGCCTCGGACTGCGACT
GCAAAAACGATGTCAATTGCAACTGCTATTCAGGAGATGATGCCTACGCGACTGATGCCATCTTGAATTCCCCATCATCC
TTAGCTGTAGCTCCAGATGGTACCATTTACATTGCAGACCTTGGAAATATTCGGATCAGGGCGGTCAGCAAGAACAAGCC
TGTTCTTAATGCCTTCAACCAGTATGAGGCTGCATCCCCCGGAGAGCAGGAGTTATATGTTTTCAACGCTGATGGCATCC
ACCAATACACTGTGAGCCTGGTGACAGGGGAGTACTTGTACAATTTCACATATAGTACTGACAATGATGTCACTGAATTG
ATTGACAATAATGGGAATTCCCTGAAGATCCGTCGGGACAGCAGTGGCATGCCCCGTCACCTGCTCATGCCTGACAACCA
GATCATCACCCTCACCGTGGGCACCAATGGAGGCCTCAAAGTCGTGTCCACACAGAACCTGGAGCTTGGTCTCATGACCT
ATGATGGCAACACTGGGCTCCTGGCCACCAAGAGCGATGAAACAGGATGGACGACTTTCTATGACTATGACCACGAAGGC
CGCCTGACCAACGTGACGCGCCCCACGGGGGTGGTAACCAGTCTGCACCGGGAAATGGAGAAATCTATTACCATTGACAT
TGAGAACTCCAACCGTGATGATGACGTCACTGTCATCACCAACCTCTCTTCAGTAGAGGCCTCCTACACAGTGGTACAAG
ATCAAGTTCGGAACAGCTACCAGCTCTGTAATAATGGTACCCTGAGGGTGATGTATGCTAATGGGATGGGTATCAGCTTC
CACAGCGAGCCCCATGTCCTAGCGGGCACCATCACCCCCACCATTGGACGCTGCAACATCTCCCTGCCTATGGAGAATGG
CTTAAACTCCATTGAGTGGCGCCTAAGAAAGGAACAGATTAAAGGCAAAGTCACCATCTTTGGCAGGAAGCTCCGGGTCC
ATGGAAGAAATCTCTTGTCCATTGACTATGATCGAAATATTCGGACTGAAAAGATCTATGATGACCACCGGAAGTTCACC
CTGAGGATCATTTATGACCAGGTGGGCCGCCCCTTCCTCTGGCTGCCCAGCAGCGGGCTGGCAGCTGTCAACGTGTCATA
CTTCTTCAATGGGCGCCTGGCTGGGCTTCAGCGTGGGGCCATGAGCGAGAGGACAGACATCGACAAGCAAGGCCGCATCG
TGTCCCGCATGTTCGCTGACGGGAAAGTGTGGAGCTACTCCTACCTTGACAAGTCCATGGTCCTCCTGCTTCAGAGCCAA
CGTCAGTATATATTTGAGTATGACTCCTCTGACCGCCTCCTTGCCGTCACCATGCCCAGCGTGGCCCGGCACAGCATGTC
CACACACACCTCCATCGGCTACATCCGTAATATTTACAACCCGCCTGAAAGCAATGCTTCGGTCATCTTTGACTACAGTG
ATGACGGCCGCATCCTGAAGACCTCCTTTTTGGGCACCGGACGCCAGGTGTTCTACAAGTATGGAAACTCTCCAAGTTA
TCAGAGATTGTCTACGACAGTACCGCCGTCACCTTCGGGTATGACGAGACCACTGGTGTCTTGAAGATGGTCAACCTCCA
AAGTGGGGGCTTCTCCTGCACCATCAGGTACCGGAAGATTGGCCCCCTGGTGGACAAGCAGATCTACAGGTTCTCCGAGG
AAGGCATGGTCAATGCCAGGTTTGACTACACCTATCATGACAACAGCTTCCGCATCGCAAGCATCAAGCCCGTCATAAGT
GAGACTCCCCTCCCCGTTGACCTCTACCGCTATGATGAGATTTCTGGCAAGGTGGAACACTTTGGTAAGTTTGGAGTCAT
CTATTATGACATCAACCAGATCATCACCACTGCCGTGATGACCCTCAGCAAACACTTCGACACCCATGGGCGGATCAAGG
AGGTCCAGTATGAGATGTTCCGGTCCCTCATGTACTGGATGACGGTGCAATATGACAGCATGGGCAGGGTGATCAAGAGG
GAGCTAAAACTGGGGCCCTATGCCAATACCACGAAGTACACCTATGACTACGATGGGGACGGGCAGCTCCAGAGCGTGGC
CGTCAATGACCGCCCGACCTGGCGCTACAGCTATGACCTTAATGGGAATCTCCACTTACTGAACCCAGGCAACAGTGTGC
GCCTCATGCCCTTGCGCTATGACCTCCGGGATCGGATAACCAGACTCGGGGATGTGCAGTACAAAATTGACGACGATGGC
TATCTGTGCCAGAGAGGGTCTGACATCTTCGAATACAATTCCAAGGGCCTCCTAACAAGAGCCTACAACAAGGCCAGCGG
GTGGAGTGTCCAGTACCGCTATGATGGCGTAGGACGGCGGGCTTCCTACAAGACCAACCTGGGCCACCACCTGCAGTACT
TCTACTCTGACCTCCACAACCCGACGCGCATCACCCATGTCTACAATCACTCCAACTCGGAGATTACCTCACTGTACTAC
GACCTCCAGGGCCACCTCTTTGCCATGGAGAGCAGCAGTGGGGAGGAGTACTATGTTGCCTCTGATAACACAGGGACTCC
TCTGGCTGTGTTCAGCATCAACGGCCTCATGATCAAACAGCTGCAGTACACGGCCTATGGGGAGATTTATTATGACTCCA
ACCCCGACTTCCAGATGGTCATTGGCTTCCATGGGGGACTCTATGACCCCCTGACCAAGCTGGTCCACTTCACTCAGCGT
GATTATGATGTGCTGGCAGGACGATGGACCTCCCCAGACTATACCATGTGGAAAAACGTGGGCAAGGAGCCGGCCCCCTT
TAACCTGTATATGTTCAAGAGCAACAATCCTCTCAGCAGTGAGCTAGATTTGAAGAACTACGTGACAGATGTGAAAAGCT
GGCTTGTGATGTTTGGATTTCAGCTTAGCAACATCATTCCTGGCTTCCCGAGAGCCAAAATGTATTTCGTGCCTCCTCCC
TATGAATTGTCAGAGAGTCAAGCAAGTGAGAATGGACAGCTCATTACAGGTGTCCAACAGACAACAGAGAGACATAACCA

GGCCTTCATGGCTCTGGAAGGACAGGTCATTACTAAAAAGCTCCACGCCAGCATCCGAGAGAAAGCAGGTCACTGGTTTG
CCACCACCACGCCCATCATTGGCAAAGGCATCATGTTTGCCATCAAAGAAGGGCGGGTGACCACGGGCGTGTCCAGCATC
GCCAGCGAAGATAGCCGCAAGGTGGCATCTGTGCTGAACAACGCCTACTACCTGGACAAGATGCACTACAGCATCGAGGG
CAAGGACACCCACTACTTTGTGAAGATTGGCTCAGCCGATGGCGACCTGGTCACACTAGGCACCACCATCGGCCGCAAGG
TGCTAGAGAGCGGGGTGAACGTGACCGTGTCCCAGCCCACGCTGCTGGTCAACGGCAGGACTCGAAGGTTCACGAACATT
GAGTTCCAGTACTCCACGCTGCTGCTCAGCATCCGCTATGGCCTCACCCCCGACACCCTGGACGAAGAGAAGGCCCGCGT
CCTGGACCAGGCGAGACAGAGGGCCCTGGGCACGGCCTGGGCCAAGGAGCAGCAGAAAGCCAGGGACGGGAGAGAGGGGA
GCCGCCTGTGGACTGAGGGCGAGAAGCAGCAGCTTCTGAGCACCGGGCGCGTGCAAGGGTACGAGGGATATTACGTGCTT
CCCGTGGAGCAATACCCAGAGCTTGCAGACAGTAGCAGCAACATCCAGTTTTTAAGACAGAATGAGATGGAAAGAGG**TA**
ACAAAATAATCTGCTGCCATTCCTTGTCTGAATGGCTCAGCAGGAGTAACTGTTATCTCCTCTCCTAAGGAGATGAAGAC
CTAACAGGGGCACTGCGGCTGGGCTGCTTTAGGAGACCAAGTGGCAAGAAAGCTCACATTTTTTGAGTTCAAATGCTACT
GTCCAAGCGAGAAGTCCCTCATCCTGAAGTAGACTAAAGCCCGGCTGAAAATTCCGAGGAAAACAAAACAAACGAATGAA
TGAACAGACACACACAATGTTCCAAGTTCCCCTAAAATATGACCCACTTGTTCTGGGTCTACGCAGAAAAGAGACGCAAA
GTGTCCAAAAGGAACAAAAGAACAAAAACGAATAAGCAAAGAAGAAAACAAACAAAAACAAAACAAAACAAACACACGGA
CCGATAAACAAAGAAGCGAAGATAAGAAAGAAGGCCTCATATCCAATTACCTCACTCATTCACATGTGAGCGACACGCAG
ACATCCGCGAGGGCCAGCGTCACCAGACCAGCTGCGGGACAAACCACTCAGACTGCTTGTAGGACAAATACTTCTGACAT
TTTCGTTTAAGCAAATACAGGTGCATTTAAAACACGACTTTGGGGGTGATTTGTGTGTAGCGCCTGGGGAGGGGGGATAA
AAGAGGAGGAGTGAGCACTGGAAATACTTTTTAAAGAAAAAAAAACATGAGGGAATAAAAGAAATTCCTATCAAAAATCA
AAGTGAAATAATACCATCCAGCACTTAACTCTCAGGTCCCAACTAAGTCTGGCCTGAGCTAATTTATTTGAGCGCAGAGT
GTAAAATTTAATTCAAAATGGTGGCTATAATCACTACAGATAAATTTCATACTCTTTTGTCTTTGGAGATTCCATTGTGG
ACAGTAATACGCAGTTACAGGGTGTAGTCTGTTTAGATTCCGTAGTTCGTGGGTATCAGTTTCGGTAGAGGTGCAGCATC
GTGACACTTTTGCTAACAGGTACCACTTCTGATCACCCTGTACATACATGAGCCGAAAGGCACAATCACTGTTTCAGATT
TAAAATTATTAGTGTGTTTGTTTGGTCCAGAAACTGAGACAATCACATGACAGTCACCACGAGGAGAGAAAATTTAAAAA
ATAAAAATAAAAACAAAAAAAATTTAAAAATTAAAAAAACAAAAATAAAGTCTAATAAGAACTTTGGTACAGGAACTTT
TTTGTAATATACATGTATGAATTGTTCATCGAGTTTTATATTAATTTTAATTTGCTGCTAAGCAAAGACTAGGGACAGG
CAAAGATAATTTATGGCAAAGTGTTTAAATTGTTTATACATAAATAAAGTCTCTAAAACTCCTGTG

The FCTR3b polypeptide (SEQ ID NO:8) encoded by SEQ ID NO:7 is 2733 amino acid residues and is presented using the one-letter code in Table 3D. The protein has a predicted molecular weight of 303424.3 daltons.

Table 3D. Encoded FCTR3b protein sequence (SEQ ID NO:8).

MDVKDRRHRSLTRGRCGKECRYTSSSLDSEDCRVPTQKSYSSSETLKAYDHDSRMHYGNRVTDLIHRESDEFPRQGTNFTLAELGI
CEPSPHRSGYCSDMGILHQGYSLSTGSDADSDTEGGMSPEHAIRLWGRGIKSRRSSGLSSRENSALTLTDSDNENKSDDENGRPIP
PTSSPSLLPSAQLPSSHNPPPVSCQMPLLDSNTSHQIMDTNPDEEFSPNSYLLRACSGPQQASSSGPPNHHSQSTLRPPLPPPHNH
TLSHHHSSANSLNRNSLTNRRSQIHAPAPAPNDLATTPESVQLQDSWVLNSNVPLETRHFLFKTSSGSTPLFSSSSPGYPLTSGTV
YTPPPRLLPRNTFSRKAFKLKKPSKYCSWKCAALSAIAAALLLAILLAYFIVPWSLKNSSIDSGEAEVGRRVTQEVPPGVFWRSQI
HISQPQFLKFNISLGKDALFGVYIRRGLPPSHAQYDFMERLDGKEKWSVVESPRERRSIQTLVQNEAVFVQYLDVGLWHLAFYNDG
KDKEMVSFNTVVLDSVQDCPRNCHGNGECVSGVCHCFPGFLGADCAKAACPVLCSGNGQYSKGTCQCYSGWKGAECDVPMNQCIDP
SCGGHGSCIDGNCVCSAGYKGEHCEEVDCLDPTCSSHGVCVNGECLCSPGWGGLNCELARVQCPDQCSGHGTYLPDTGLCSCDPNW
MGPDCSVEVCSVDCGTHGVCIGGACRCEEGWTGAACDQRVCHPRCIEHGTCKDGKCECREGWNGEHCTIGRQTAGTETDGCPDLCN
GNGRCTLGQNSWQCVCQTGWRGPGCNVAMETSCADNKDNEGDGLVDCLDPDCCLQSACQNSLLCRGSRDPLDIIQQGQTDWPAVKS
FYDRIKLLAGKDSTHIIPGENPFNSSLVSLIRGQVVTTDGTPLVGVNVSFVKYPKYGYTITRQDGTFDLIANGGASLTLHFERAPF
MSQERTVWLPWNSFYAMDTLVMKTEENSIPSCDLSGFVRPDPIIISSPLSTFFSAAPGQNPIVPETQVLHEEIELPGSNVKLRYLS
SRTAGYKSLLKITMTQSTVPLNLIRVHLMVAVEGHLFQKSFQASPNLASTFIWDKTDAYGQRVYGLSDAVVSVGFEYETCPSLILW
EKRTALLQGFELDPSNLGGWSLDKHHILNVKSGILHKGTGENQFLTQQPAIITSIMGNGRRRSISCPSCNGLAEGNKLLAPVALAV
GIDGSLYVGDFNYIRRIFPSRNVTSILELRNKEFKHSNNPAHKYYLAVDPVSGSLYVSDTNSRRIYRVKSLSGTKDLAGNSEVVAG
TGEQCLPFDEARCGDGGKAIDATLMSPRGIAVDKNGLMYFVDATMIRKVDQNGIISTLLGSNDLTAVRPLSCDSSMDVAQVRLEWP
TDLAVNPMDNSLYVLENNVILRITENHQVSIIAGRPMHCQVPGIDYSLSKLAIHSALESASAIAISHTGVLYITETDEKKINRLRQ
VTTNGEICLLAGAASDCDCKNDVNCNCYSGDDAYATDAILNSPSSLAVAPDGTIYIADLGNIRIRAVSKNKPVLNAFNQYEAASPG
EQELYVFNADGIHQYTVSLVTGEYLYNFTYSTDNDVTELIDNNGNSLKIRRDSSGMPRHLLMPDNQIITLTVGTNGGLKVVSTQNL
ELGLMTYDGNTGLLATKSDETGWTTFYDYDHEGRLTNVTRPTGVVTSLHREMEKSITIDIENSNRDDDVTVITNLSSVEASYTVVQ
DQVRNSYQLCNNGTLRVMYANGMGISFHSEPHVLAGTITPTIGRCNISLPMENGLNSIEWRLRKEQIKGKVTIFGRKLRVHGRNLL
SIDYDRNIRTEKIYDDHRKFTLRIIYDQVGRPFLWLPSSGLAAVNVSYFFNGRLAGLQRGAMSERTDIDKQGRIVSRMFADGKVWS
YSYLDKSMVLLLQSQRQYIFEYDSSDRLLAVTMPSVARHSMSTHTSIGYIRNIYNPPESNASVIFDYSDDGRILKTSFLGTGRQVF
YKYGKLSKLSEIVYDSTAVTFGYDETTGVLKMVNLQSGGFSCTIRYRKIGPLVDKQIYRFSEEGMVNARFDYTYHDNSFRIASIKP
VISETPLPVDLYRYDEISGKVEHFGKFGVIYYDINQIITTAVMTLSKHFDTHGRIKEVQYEMFRSLMYWMTVQYDSMGRVIKRELK
LGPYANTTKYTYDYDGDGQLQSVAVNDRPTWRYSYDLNGNLHLLNPGNSVRLMPLRYDLRDRITRLGDVQYKIDDDGYLCQRGSDI
FEYNSKGLLTRAYNKASGWSVQYRYDGVGRRASYKTNLGHHLQYFYSDLHNPTRITHVYNHSNSEITSLYYDLQGHLFAMESSSGE
EYYVASDNTGTPLAVFSINGLMIKQLQYTAYGEIYYDSNPDFQMVIGFHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWKNVG
KEPAPFNLYMFKSNNPLSSELDLKNYVTDVKSWLVMFGFQLSNIIPGFPRAKMYFVPPPYELSESQASENGQLITGVQQTTERHNQ
AFMALEGQVITKKLHASIREKAGHWFATTTPIIGKGIMFAIKEGRVTTGVSSIASEDSRKVASVLNNAYYLDKMHYSIEGKDTHYF
VKIGSADGDLVTLGTTIGRKVLESGVNVTVSQPTLLVNGRTRRFTNIEFQYSTLLLSIRYGLTPDTLDEEKARVLDQARQRALGTA
WAKEQQKARDGREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADSSSNIQFLRQNEMGKR

In further alternative embodiments the italicized bases in the 5' end of the FCTR3b sequence in table 3C is a variable region. This region can be substituted for in other embodiments of FCTR3. The nucleotide sequence for 9823bp FCTR3c (also referred to herein as 10129612.0.154) has the same nucleotide sequence as FCTR3b except that the italicized region is replaced with the 201 base sequence shown in Table 3E. An ORF for the total FCTR3c nucleotide sequence was identified beginning with an ATG initiation codon at nucleotides 277-280 and ending with a TAG codon at nucleotides 8473-8475. This is the same open reading frame that is shown in Table 3C, with the corresponding base numbers for FCTR3c. This open reading frame will translate the same amino acid sequence as shown in Table 3C for FCTR3b.

Table 3E. Encoded FCTR3c 5'end nucleotide sequence (SEQ ID NO:9).

GCTCCAAAGCGAGCTGGGACCGAAGACTCTAGGCTAAGTTATCTATGTAGATGGTGTCAGGGAGCGAAGCTACTGACCGA
GCTGCTGTTACATCCAGCTTTTTAATTGCCTAAGCGGTCTGGGGCTTGCTTCGTCATTTGGCTTTGCTGTGGAGCACTCC
TGTAAAGCCAGCTGAATTGTACATCGAAGATCCACCCTTTT

In yet another embodiment, the italicized region shown in the 5' end of the sequence in Table 3C can be replaced with the sequence shown in Table 3F to form 9823bp FCTR3d (also referred to herein as 10129612.0.67). An ORF was identified beginning with an ATG initiation codon at nucleotides 277-280 and ending with a TAG codon at nucleotides 8473-8475. This is the same open reading frame that is shown in Table 3C, with the corresponding base numbers for FCTR3d. This open reading frame will translate the same amino acid sequence as shown in Table 3D for FCTR3b.

Table 3F. Encoded FCTR3d 5'end nucleotide sequence (SEQ ID NO:10).

GCTCCAAAGCGAGCTGGGACCGAAGACTCTAGGCTAAGTTATCTATGTAGATGGTGTCAGGGAGCGAAGCTACTGACCGA
GCTGCTGTTACATCCAGCTTTTTAATTGCCTAAGCGGTCTGGGGCTTGCTTCGTCATTTGGCTTTGCTGTGGAGCACTCC
TGTAAAGCCAGCTGAATTGTACATCGAAGATCCACCCTTTT

In yet another embodiment, the italicized region shown in the 5' end of the sequence in Table 3C can be replaced with the sequence shown in Table 3G to form 9765 bp FCTR3e (also referred to as 10129612.0.258). An ORF was identified beginning with an ATG initiation codon at nucleotides 210-212 and ending with a TAG codon at nucleotides 8408-8410. This is the same open reading frame that is shown in Table 3C, with the corresponding base numbers for FCTR3e. This open reading frame will translate the same amino acid sequence as shown in Table 3D for FCTR3b.

Table 3G. Encoded FCTR3e 5'end nucleotide sequence (SEQ ID NO:11).

CCAGCATTAGATGAGTTGACAAAAATGCAGTTTCAGCTCTGAAGGTCTGAAAGATTCTGCTGCAACTAAAGCTCTGAAGA
TTCTGCTACAACTATGACATCCATTTTCTCCCACTTCAGACAGGATGAATACAA

In yet another embodiment another FCTR3a homolog, FCTR3f (also referred to as 10129612.0.352) was found having the 9729bp sequence shown in Table 3H. An ORF was identified beginning with an ATG initiation codon at nucleotides 210-212 and ending with a TAG codon at nucleotides 8382-8384. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 3G, and the start and stop codons are in bold letters.

Table 3H. Encoded FCTR3f nucleotide sequence (SEQ ID NO:12).

CCAGCATTAGATGAGTTGACAAAAATGCAGTTTCAGCTCTGAAGGTCTGAAAGATTCTGCTGCAACTAAAGCTCTGAAGA
TTCTGCTACAACTATGACATCCATTTTCTCCCACTTCAGACAGGATGAATACAAGGTGGCAAAGTGACAAGTGCCAAAAC
TCAGGCCTGACTTTCCTGAAAACATCAGCATTCTGCCATATCTGGAATA**ATG**GATGTAAAGGACCGGCGACACCGCTCTT
TGACCAGAGGACGCTGTGGCAAAGAGTGTCGCTACACAAGCTCCTCTCTGGACAGTGAGGACTGCCGGGTGCCCACACAG
AAATCCTACAGCTCCAGTGAGACTCTGAAGGCCTATGACCATGACAGCAGGATGCACTATGGAAACCGAGTCACAGACCT
CATCCACCGGGAGTCAGATGAGTTTCCTAGACAAGGAACCAACTTCACCCTTGCCGAACTGGGCATCTGTGAGCCCTCCC
CACACCGAAGCGGCTACTGCTCCGACATGGGGATCCTTCACCAGGGCTACTCCCTTAGCACAGGGTCTGACGCCGACTCC
GACACCGAGGGAGGGATGTCTCCAGAACACGCCATCAGACTGTGGGGCAGAGGGATAAAATCCAGGCGCAGTTCCGGCCT
GTCCAGTCGTGAAAACTCGGCCCTTACCCTGACTGACTCTGACAACGAAAACAAATCAGATGATGAGAACGGTCGTCCCA
TTCCACCTACATCCTCGCCTAGTCTCCTCCCATCTGCTCAGCTGCCTAGCTCCCATAATCCTCCACCAGTTAGCTGCCAG
ATGCCATTGCTAGACAGCAACACCTCCCATCAAATCATGGACACCAACCCTGATGAGGAATTCTCCCCCAATTCATACCT
GCTCAGAGCATGCTCAGGGCCCCAGCAAGCCTCCAGCAGTGGCCCTCCGAACCACCACAGCCAGTCGACTCTGAGGCCCC
CTCTCCCACCCCCTCACAACCACACGCTGTCCCATCACCACTCGTCCGCCAACTCCCTCAACAGGAACTCACTGACCAAT
CGGCGGAGTCAGATCCACGCCCCGGCCCCAGCGCCCAATGACCTGGCCACCACACCAGAGTCCGTTCAGCTTCAGGACAG
CTGGGTGCTAAACAGCAACGTGCCACTGGAGACCCGGCACTTCCTCTTCAAGACCTCCTCGGGGAGCACACCCTTGTTCA
GCAGCTCTTCCCCGGGATACCCTTTGACCTCAGGAACGGTTTACACGCCCCCGCCCCGCCTGCTGCCCAGGAATACTTTC
TCCAGGAAGGCTTTCAAGCTGAAGAAGCCCTCCAAATACTGCAGCTGGAAATGTGCTGCCCTCTCCGCCATTGCCGCGGC
CCTCCTCTTGGCTATTTTGCTGGCGTATTTCATAGTGCCCTGGTCGTTGAAAAACAGCAGCATAGACAGTGGTGAAGCAG
AAGTTGGTCGGCGGGTAACACAAGAAGTCCCACCAGGGGTGTTTTGGAGGTCACAAATTCACATCAGTCAGCCCCAGTTC
TTAAAGTTCAACATCTCCCTCGGGAAGGACGCTCTCTTTGGTGTTTACATAAGAAGAGGACTTCCACCATCTCATGCCCA
GTATGACTTCATGGAACGTCTGGACGGGAAGGAGAAGTGGAGTGTGGTTGAGTCTCCCAGGGAACGCCGGAGCATACAGA
CCTTGGTTCAGAATGAAGCCGTGTTTGTGCAGTACCTGGATGTGGGCCTGTGGCATCTGGCCTTCTACAATGATGGAAAA
GACAAAGAGATGGTTTCCTTCAATACTGTTGTCCTAGATTCAGTGCAGGACTGTCCACGTAACTGCCATGGAATGGTGA
ATGTGTGTCCGGGGTGTGTCACTGTTTCCCAGGATTTCTAGGAGCAGACTGTGCTAAAGCTGCCTGCCCTGTCCTGTGCA
GTGGGAATGGACAATATTCTAAAGGACGTGCCAGTGCTACAGCGGCTGGAAAGGTGCAGAGTGCGACGTGCCCATGAAT
CAGTGCATCGATCCTTCCTGCGGGGGCCACGGCTCCTGCATTGATGGGAACTGTGTCTGCTCTGCTGGCTACAAAGGCGA
GCACTGTGAGGAAGTTGATTGCTTGGATCCCACCTGCTCCAGCCACGGAGTCTGTGTGAATGGAGAATGCCTGTGCAGCC
CTGGCTGGGGTGGTCTGAACTGTGAGCTGGCGAGGGTCCAGTGCCCAGACCAGTGCAGTGGGCATGGCACGTACCTGCCT
GACACGGGCCTCTGCAGCTGCGATCCCAACTGGATGGGTCCCGACTGCTCTGTTGAAGTGTGCTCAGTAGACTGTGGCAC
TCACGGCGTCTGCATCGGGGGAGCCTGCCGCTGTGAAGAGGGCTGGACAGGCGCAGCGTGTGACCAGCGCGTGTGCCACC
CCCGCTGCATTGAGCATGGGACCTGTAAAGATGGCAAATGTGAATGCCGAGAGGGCTGGAATGGTGAACACTGCACCATT
GATGGCTGCCCTGACTTGTGCAACGGTAACGGGAGATGCACACTGGGTCAGAACAGCTGGCAGTGTGTCTGCCAGACCGG
CTGGAGAGGGCCCGGATGCAACGTTGCCATGGAAACTTCCTGTGCTGATAACAAGGATAATGAGGGAGATGGCCTGGTGG
ATTGTTTGGACCCTGACTGCTGCCTGCAGTCAGCCTGTCAGAACAGCCTGCTCTGCCGGGGGTCCCGGGACCCACTGGAC
ATCATTCAGCAGGGCCAGACGGATTGGCCCGCAGTGAAGTCCTTCTATGACCGTATCAAGCTCTTGGCAGGCAAGGATAG
CACCCACATCATTCCTGGAGAGAACCCTTTCAACAGCAGCTTGGTTTCTCTCATCCGAGGCCAAGTAGTAACTACAGATG
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TTCGACCTGATCGCAAATGGAGGTGCTTCCTTGACTCTACACTTTGAGCGAGCCCCGTTCATGAGCCAGGAGCGCACTGT
GTGGCTGCCGTGGAACAGCTTTTACGCCATGGACACCCTGGTGATGAAGACCGAGGAGAACTCCATCCCCAGCTGTGACC
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CCTGCCATCATCACCAGCATCATGGGCAATGGTCGCCGCCGGAGCATTTCCTGTCCCAGCTGCAACGGCCTTGCTGAAGG
CAACAAGCTGCTGGCCCCAGTGGCTCTGGCTGTTGGAATCGATGGGAGCCTCTATGTGGGTGACTTCAATTACATCCGAC
GCATCTTTCCCTCTCGAAATGTGACCAGCATCTTGGAGTTACGAAATAAAGAGTTTAAACATAGCAACAACCCAGCACAC
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GTCTCTGAGTGGAACCAAAGACCTGGCTGGGAATTCGGAAGTTGTGGCAGGGACGGGAGAGCAGTGTCTACCCTTTGATG
AAGCCCGCTGCGGGGATGGAGGGAAGGCCATAGATGCAACCCTGATGAGCCCGAGAGGTATTGCAGTAGACAAGAATGGG
CTCATGTACTTTGTCGATGCCACCATGATCCGGAAGGTTGACCAGAATGGAATCATCTCCACCCTGCTGGGCTCCAATGA
CCTCACTGCCGTCCGGCCGCTGAGCTGTGATTCCAGCATGGATGTAGCCCAGGTTCGTCTGGAGTGGCCAACAGACCTTG
CTGTCAATCCCATGGATAACTCCTTGTATGTTCTAGAGAACAATGTCATCCTTCGAATCACCGAGAACCACCAAGTCAGC

ATCATTGCGGGACGCCCCATGCACTGCCAAGTTCCTGGCATTGACTACTCACTCAGCAAACTAGCCATTCACTCTGCCCT
GGAGTCAGCCAGTGCCATTGCCATTTCTCACACTGGGGTCCTCTACATCACTGAGACAGATGAGAAGAAGATTAACCGTC
TACGCCAGGTAACAACCAACGGGGAGATCTGCCTTTTAGCTGGGGCAGCCTCGGACTGCGACTGCAAAAACGATGTCAAT
TGCAACTGCTATTCAGGAGATGATGCCTACGCGACTGATGCCATCTTGAATTCCCCATCATCCTTAGCTGTAGCTCCAGA
TGGTACCATTTACATTGCAGACCTTGGAAATATTCGGATCAGGGCGGTCAGCAAGAACAAGCCTGTTCTTAATGCCTTCA
ACCAGTATGAGGCTGCATCCCCCGGAGAGCAGGAGTTATATGTTTTCAACGCTGATGGCATCCACCAATACACTGTGAGC
CTGGTGACAGGGGAGTACTTGTACAATTTCACATATAGTACTGACAATGATGTCACTGAATTGATTGACAATAATGGGAA
TTCCCTGAAGATCCGTCGGGACAGCAGTGGCATGCCCCGTCACCTGCTCATGCCTGACAACCAGATCATCACCCTCACCG
TGGGCACCAATGGAGGCCTCAAAGTCGTGTCCACACAGAACCTGGAGCTTGGTCTCATGACCTATGATGGCAACACTGGG
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GCGCCCCACGGGGGTGGTAACCAGTCTGCACCGGGAAATGGAGAAATCTATTACCATTGACATTGAGAACTCCAACCGTG
ATGATGACGTCACTGTCATCACCAACCTCTCTTCAGTAGAGGCCTCCTACACAGTGGTACAAGATCAAGTTCGGAACAGC
TACCAGCTCTGTAATAATGGTACCCTGAGGGTGATGTATGCTAATGGGATGGGTATCAGCTTCCACAGCGAGCCCCATGT
CCTAGCGGGCACCATCACCCCCACCATTGGACGCTGCAACATCTCCCTGCCTATGGAGAATGGCTTAAACTCCATTGAGT
GGCGCCTAAGAAAGGAACAGATTAAAGGCAAAGTCACCATCTTTGGCAGGAAGCTCCGGGTCCATGGAAGAAATCTCTTG
TCCATTGACTATGATCGAAATATTCGGACTGAAAAGATCTATGATGACCACCGGAAGTTCACCCTGAGGATCATTTATGA
CCAGGTGGGCCGCCCCTTCCTCTGGCTGCCCAGCAGCGGGCTGGCAGCTGTCAACGTGTCATACTTCTTCAATGGGCGCC
TGGCTGGGCTTCAGCGTGGGGCCATGAGCGAGAGGACAGACATCGACAAGCAAGGCCGCATCGTGTCCCGCATGTTCGCT
GACGGGAAAGTGTGGAGCTACTCCTACCTTGACAAGTCCATGGTCCTCCTGCTTCAGAGCCAACGTCAGTATATATTTGA
GTATGACTCCTCTGACCGCCTCCTTGCCGTCACCATGCCCAGCGTGGCCCGGCACAGCATGTCCACACACACCTCCATCG
GCTACATCCGTAATATTTACAACCCGCCTGAAAGCAATGCTTCGGTCATCTTTGACTACAGTGATGACGGCCGCATCCTG
AAGACCTCCTTTTTGGGCACCGGACGCCAGGTGTTCTACAAGTATGGGAAACTCTCCAAGTTATCAGAGATTGTCTACGA
CAGTACCGCCGTCACCTTCGGGTATGACGAGACCACTGGTGTCTTGAAGATGGTCAACCTCCAAAGTGGGGGCTTCTCCT
GCACCATCAGGTACCGGAAGATTGGCCCCCTGGTGGACAAGCAGATCTACAGGTTCTCCGAGGAAGGCATGGTCAATGCC
AGGTTTGACTACACCTATCATGACAACAGCTTCCGCATCGCAAGCATCAAGCCCGTCATAAGTGAGACTCCCCTCCCCGT
TGACCTCTACCGCTATGATGAGATTTCTGGCAAGGTGGAACACTTTGGTAAGTTTGGAGTCATCTATTATGACATCAACC
AGATCATCACCACTGCCGTGATGACCCTCAGCAAACACTTCGACACCCATGGGCGGATCAAGGAGGTCCAGTATGAGATG
TTCCGGTCCCTCATGTACTGGATGACGGTGCAATATGACAGCATGGGCAGGGTGATCAAGAGGGAGCTAAAACTGGGGCC
CTATGCCAATACCACGAAGTACACCTATGACTACGATGGGGACGGGCAGCTCCAGAGCGTGGCCGTCAATGACCGCCCGA
CCTGGCGCTACAGCTATGACCTTAATGGGAATCTCCACTTACTGAACCCAGGCAACAGTGTGCGCCTCATGCCCTTGCGC
TATGACCTCCGGGATCGGATAACCAGACTCGGGGATGTGCAGTACAAAATTGACGACGATGGCTATCTGTGCCAGAGAGG
GTCTGACATCTTCGAATACAATTCCAAGGGCCTCCTAACAAGAGCCTACAACAAGGCCAGCGGGTGGAGTGTCCAGTACC
GCTATGATGGCGTAGGACGGCGGGCTTCCTACAAGACCAACCTGGGCCACCACCTGCAGTACTTCTACTCTGACCTCCAC
AACCCGACGCGCATCACCCATGTCTACAATCACTCCAACTCGGAGATTACCTCACTGTACTACGACCTCCAGGGCCACCT
CTTTGCCATGGAGAGCAGCAGTGGGGAGGAGTACTATGTTGCCTCTGATAACACAGGGACTCCTCTGGCTGTGTTCAGCA
TCAACGGCCTCATGATCAAACAGCTGCAGTACACGGCCTATGGGGAGATTTATTATGACTCCAACCCCGACTTCCAGATG
GTCATTGGCTTCCATGGGGGACTCTATGACCCCCTGACCAAGCTGGTCCACTTCACTCAGCGTGATTATGATGTGCTGGC
AGGACGATGGACCTCCCCAGACTATACCATGTGGAAAAACGTGGGCAAGGAGCCGGCCCCCTTTAACCTGTATATGTTCA
AGAGCAACAATCCTCTCAGCAGTGAGCTAGATTTGAAGAACTACGTGACAGATGTGAAAAGCTGGCTTGTGATGTTTGGA
TTTCAGCTTAGCAACATCATTCCTGGCTTCCCGAGAGCCAAAATGTATTTCGTGCCTCCTCCCTATGAATTGTCAGAGAG
TCAAGCAAGTGAGAATGGACAGCTCATTACAGGTGTCCAACAGACAACAGAGAGACATAACCAGGCCTTCATGGCTCTGG
AAGGACAGGTCATTACTAAAAAGCTCCACGCCAGCATCCGAGAGAAAGCAGGTCACTGGTTTGCCACCACCACGCCCATC
ATTGGCAAAGGCATCATGTTTGCCATCAAAGAAGGGCGGGTGACCACGGGCGTGTCCAGCATCGCCAGCGAAGATAGCCG
CAAGGTGGCATCTGTGCTGAACAACGCCTACTACCTGGACAAGATGCACTACAGCATCGAGGGCAAGGACACCCACTACT
TTGTGAAGATTGGCTCAGCCGATGGCGACCTGGTCACACTAGGCACCACCATCGGCCGCAAGGTGCTAGAGAGCGGGGTG
AACGTGACCGTGTCCCAGCCCACGCTGCTGGTCAACGGCAGGACTCGAAGGTTCACGAACATTGAGTTCCAGTACTCCAC
GCTGCTGCTCAGCATCCGCTATGGCCTCACCCCCGACACCCTGGACGAAGAGAAGGCCCGCGTCCTGGACCAGGCGAGAC
AGAGGGCCCTGGGCACGGCCTGGGCCAAGGAGCAGCAGAAAGCCAGGGACGGGAGAGAGGGGAGCCGCCTGTGGACTGAG
GGCGAGAAGCAGCAGCTTCTGAGCACCGGGCGCGTGCAAGGGTACGAGGGATATTACGTGCTTCCCGTGGAGCAATACCC
AGAGCTTGCAGACAGTAGCAGCAACATCCAGTTTTTAAGACAGAATGAGATGGGAAAGAGG**TAA**CAAAATAATCTGCTGC
CATTCCTTGTCTGAATGGCTCAGCAGGAGTAACTGTTATCTCCTCTCCTAAGGAGATGAAGACCTAACAGGGGCACTGCG
GCTGGGCTGCTTTAGGAGACCAAGTGGCAAGAAAGCTCACATTTTTTGAGTTCAAATGCTACTGTCCAAGCGAGAAGTCC
CTCATCCTGAAGTAGACTAAAGCCCGGCTGAAAATTCCGAGGAAAACAAAACAAACGAATGAATGAACAGACACACACAA
TGTTCCAAGTTCCCCTAAAATATGACCCACTTGTTCTGGGTCTACGCAGAAAAGAGACGCAAAGTGTCCAAAAGGAACAA
AAGAACAAAAACGAATAAGCAAAGAAGAAAACAAACAAAAACAAAACAAAACAAACACACGGACCGATAAACAAAGAAGC
GAAGATAAGAAAGAAGGCCTCATATCCAATTACCTCACTCATTCACATGTGAGCGACACGCAGACATCCGCGAGGGCCAG
CGTCACCAGACCAGCTGCGGGACAAACCACTCAGACTGCTTGTAGGACAAATACTTCTGACATTTTCGTTTAAGCAAATA
CAGGTGCATTTAAAACACGACTTTGGGGGTGATTTGTGTGTAGCGCCTGGGGAGGGGGGATAAAAGAGGAGGAGTGAGCA
CTGGAAATACTTTTTAAAGAAAAAAAAACATGAGGGAATAAAAGAAATTCCTATCAAAAATCAAAGTGAAATAATACCAT
CCAGCACTTAACTCTCAGGTCCCAACTAAGTCTGGCCTGAGCTAATTTATTTGAGCGCAGAGTGTAAAATTTAATTCAAA
ATGGTGGCTATAATCACTACAGATAAATTTCATACTCTTTTGTCTTTGGAGATTCCATTGTGGACAGTAATACGCAGTTA
CAGGGTGTAGTCTGTTTAGATTCCGTAGTTCGTGGGTATCAGTTTCGGTAGAGGTGCAGCATCGTGACACTTTTGCTAAC
AGGTACCACTTCTGATCACCCTGTACATACATGAGCCGAAAGGCACAATCACTGTTTCAGATTTAAAATTATTAGTGTGT
TTGTTTGGTCCAGAAACTGAGACAATCACATGACAGTCACCACGAGGAGAGAAAATTTAAAAAATAAAAATAAAAACAAA
AAAAATTTAAAAATTAAAAAAACAAAAATAAAGTCTAATAAGAACTTTGGTACAGGAACTTTTTTGTAATATACATGTA
TGAATTGTTCATCGAGTTTTTATATTAATTTTAATTTGCTGCTAAGCAAAGACTAGGGACAGGCAAAGATAATTTATGGC
AAAGTGTTTAAATTGTTTATACATAAATAAAGTCTCTAAAACTCCTGTG

The FCTR3f polypeptide (SEQ ID NO:13) encoded by SEQ ID NO:12 is 2724 amino acid residues long and is presented using the one-letter code in Table 3I. This sequence differs from FCTR3b in that it is missing amino acids 758-766 from that polypeptide.

Table 3I. Encoded FCTR3f protein sequence (SEQ ID NO:13)

```
MDVKDRRHRSLTRGRCGKECRYTSSSLDSEDCRVPTQKSYSSSETLKAYDHDSRMHYGNRVTDLIHRESDEFPRQGTNFTLAELGI
CEPSPHRSGYCSDMGILHQGYSLSTGSDADSDTEGGMSPEHAIRLWGRGIKSRRSSGLSSRENSALTLTDSDNENKSDDENGRPIP
PTSSPSLLPSAQLPSSHNPPPVSCQMPLLDSNTSHQIMDTNPDEEFSPNSYLLRACSGPQQASSSGPPNHHSQSTLRPPLPPPHNH
TLSHHHSSANSLNRNSLTNRRSQIHAPAPAPNDLATTPESVQLQDSWVLNSNVPLETRHFLFKTSSGSTPLFSSSSPGYPLTSGTV
YTPPPRLLPRNTFSRKAFKLKKPSKYCSWKCAALSAIAAALLLAILLAYFIVPWSLKNSSIDSGEAEVGRRVTQEVPPGVFWRSQI
HISQPQFLKFNISLGKDALFGVYIRRGLPPSHAQYDFMERLDGKEKWSVVESPRERRSIQTLVQNEAVFVQYLDVGLWHLAFYNDG
KDKEMVSFNTVVLDSVQDCPRNCHGNGECVSGVCHCFPGFLGADCAKAACPVLCSGNGQYSKGTCQCYSGWKGAECDVPMNQCIDP
SCGGHGSCIDGNCVCSAGYKGEHCEEVDCLDPTCSSHGVCVNGECLCSPGWGGLNCELARVQCPDQCSGHGTYLPDTGLCSCDPNW
MGPDCSVEVCSVDCGTHGVCIGGACRCEEGWTGAACDQRVCHPRCIEHGTCKDGKCECREGWNGEHCTIDGCPDLCNGNGRCTLGQ
NSWQCVCQTGWRGPGCNVAMETSCADNKDNEGDGLVDCLDPDCCLQSACQNSLLCRGSRDPLDIIQQGQTDWPAVKSFYDRIKLLA
GKDSTHIIPGENPFNSSLVSLIRGQVVTTDGTPLVGVNVSFVKYPKYGYTITRQDGTFDLIANGGASLTLHFERAPFMSQERTVWL
PWNSFYAMDTLVMKTEENSIPSCDLSGFVRPDPIIISSPLSTFFSAAPGQNPIVPETQVLHEEIELPGSNVKLRYLSSRTAGYKSL
LKITMTQSTVPLNLIRVHLMVAVEGHLFQKSFQASPNLASTFIWDKTDAYGQRVYGLSDAVVSVGFEYETCPSLILWEKRTALLQG
FELDPSNLGGWSLDKHHILNVKSGILHKGTGENQFLTQQPAIITSIMGNGRRRSISCPSCNGLAEGNKLLAPVALAVGIDGSLYVG
DFNYIRRIFPSRNVTSILELRNKEFKHSNNPAHKYYLAVDPVSGSLYVSDTNSRRIYRVKSLSGTKDLAGNSEVVAGTGEQCLPFD
EARCGDGGKAIDATLMSPRGIAVDKNGLMYFVDATMIRKVDQNGIISTLLGSNDLTAVRPLSCDSSMDVAQVRLEWPTDLAVNPMD
NSLYVLENNVILRITENHQVSIIAGRPMHCQVPGIDYSLSKLAIHSALESASAIAISHTGVLYITETDEKKINRLRQVTTNGEICL
LAGAASDCDCKNDVNCNCYSGDDAYATDAILNSPSSLAVAPDGTIYIADLGNIRIRAVSKNKPVLNAFNQYEAASPGEQELYVFNA
DGIHQYTVSLVTGEYLYNFTYSTDNDVTELIDNNGNSLKIRRDSSGMPRHLLMPDNQIITLTVGTNGGLKVVSTQNLELGLMTYDG
NTGLLATKSDETGWTTFYDYDHEGRLTNVTRPTGVVTSLHREMEKSITIDIENSNRDDDVTVITNLSSVEASYTVVQDQVRNSYQL
CNNGTLRVMYANGMGISFHSEPHVLAGTITPTIGRCNISLPMENGLNSIEWRLRKEQIKGKVTIFGRKLRVHGRNLLSIDYDRNIR
TEKIYDDHRKFTLRIIYDQVGRPFLWLPSSGLAAVNVSYFFNGRLAGLQRGAMSERTDIDKQGRIVSRMFADGKVWSYSYLDKSMV
LLLQSQRQYIFEYDSSDRLLAVTMPSVARHSMSTHTSIGYIRNIYNPPESNASVIFDYSDDGRILKTSFLGTGRQVFYKYGKLSKL
SEIVYDSTAVTFGYDETTGVLKMVNLQSGGFSCTIRYRKIGPLVDKQIYRFSEEGMVNARFDYTYHDNSFRIASIKPVISETPLPV
DLYRYDEISGKVEHFGKFGVIYYDINQIITTAVMTLSKHFDTHGRIKEVQYEMFRSLMYWMTVQYDSMGRVIKRELKLGPYANTTK
YTYDYDGDGQLQSVAVNDRPTWRYSYDLNGNLHLLNPGNSVRLMPLRYDLRDRITRLGDVQYKIDDDGYLCQRGSDIFEYNSKGLL
TRAYNKASGWSVQYRYDGVGRRASYKTNLGHHLQYFYSDLHNPTRITHVYNHSNSEITSLYYDLQGHLFAMESSSGEEYYVASDNT
GTPLAVFSINGLMIKQLQYTAYGEIYYDSNPDFQMVIGFHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWKNVGKEPAPFNLY
MFKSNNPLSSELDLKNYVTDVKSWLVMFGFQLSNIIPGFPRAKMYFVPPPYELSESQASENGQLITGVQQTTERHNQAFMALEGQV
ITKKLHASIREKAGHWFATTTPIIGKGIMFAIKEGRVTTGVSSIASEDSRKVASVLNNAYYLDKMHYSIEGKDTHYFVKIGSADGD
LVTLGTTIGRKVLESGVNVTVSQPTLLVNGRTRRFTNIEFQYSTLLLSIRYGLTPDTLDEEKARVLDQARQRALGTAWAKEQQKAR
DGREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADSSSNIQFLRQNEMGKR
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In a BLASTN search it was found that the FCTR3a nucleic acid has homology to three fragments of *Mus musculus* odd Oz/ten-m homolog 2. It has 634 of 685 bases (92%) identical to bases 614-1298, 365 of 406 bases (89%) identical to bases 1420-1825, and 93 of 103 bases (90%) identical to bases 1823-1925 of *Mus musculus* odd Oz/ten-m homolog 2 (GenBank Acc: NM_011856.2) (Table 3J).

Table 3J. BLASTN of FCTR3a against *Mus musculus* odd Oz/ten-m homolog 2 (SEQ ID NO:62)

```
>GI|7657414|REF|NM_011856.2| MUS MUSCULUS ODD OZ/TEN-M HOMOLOG 2 (DROSOPHILA) (ODZ2),
MRNA
          LENGTH = 8797

 SCORE =  954 BITS (481), EXPECT = 0.0
 IDENTITIES = 634/685 (92%)
 STRAND = PLUS / PLUS

QUERY: 114  GGTCGTCCCATTCCACCTACATCCTCGCCTAGTCTCCTCCCATCTGCTCAGCTGCCTAGC 173
            |||||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||
SBJCT: 614  GGTCGTCCCATTCCACCTACATCCTCGTCTAGCCTCCTCCCATCTGCTCAGCTGCCTAGC 673
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QUERY: 174   TCCCATAATCCTCCACCAGTTAGCTGCCAGATGCCATTGCTAGACAGCAACACCTCCCAT 233
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 674   TCCCATAATCCTCCACCAGTTAGCTGCCAGATGCCATTGCTAGACAGCAACACCTCCCAT 733

QUERY: 234   CAAATCATGGACACCAACCCTGATGAGGAATTCTCCCCAATTCATACCTGCTCAGAGCA 293
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 734   CAGATCATGGACACCAACCCTGATGAGGAATTCTCCCCAATTCATACCTGCTCAGAGCA 793

QUERY: 294   TGCTCAGGGCCCCAGCAAGCCTCCAGCAGTGGCCCTCCGAACCACCACAGCCAGTCGACT 353
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||||| || 
SBJCT: 794   TGCTCAGGGCCCCAGCAAGCCTCCAGCAGTGGCCCTCCAAACCACCACAGCCAGTCAACA 853

QUERY: 354   CTGAGGCCCCCTCTCCCACCCCCTCACAACCACACGCTGTCCCATCACCACTCGTCCGCC 413
             |||||||||||||| ||||||||||| |||||||| |||||||| |||||||| || |||
SBJCT: 854   CTGAGGCCCCCTCTGCCACCCCCTCATAACCACACCCTGTCCCACCACCACTCCTCGGCC 913

QUERY: 414   AACTCCCTCAACAGGAACTCACTGACCAATCGGCGGAGTCAGATCCACGCCCCGGCCCCA 473
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||| || || 
SBJCT: 914   AACTCCCTCAACAGGAACTCACTGACCAATCGGCGGAGTCAAATCCACGCCCCAGCTCCT 973

QUERY: 474   GCGCCCAATGACCTGGCCACCACACCAGAGTCCGTTCAGCTTCAGGACAGCTGGGTGCTA 533
             |||||||| |||||||||||||| |||||||| |||||||| ||||| ||||||||||| 
SBJCT: 974   GCGCCCAACGACCTGGCCACCACCCCAGAGTCTGTTCAGCTCCAGGATAGCTGGGTGCTG 1033

QUERY: 534   AACAGCAACGTGCCACTGGAGACCCGGCACTTCCTCTTCAAGACCTCCTCGGGGAGCACA 593
             ||||| ||||| ||||||||||| ||||||||||| ||||| || || || || ||||||
SBJCT: 1034  AACAGTAACGTCCCACTGGAGACTCGGCACTTCCTTTTCAAAACGTCGTCTGGAAGCACA 1093

QUERY: 594   CCCTTGTTCAGCAGCTCTTCCCCGGGATACCCTTTGACCTCAGGAACGGTTTACACGCCC 653
             ||| |||||||||||||||| ||||||||||||||||||||||| || ||||| || || 
SBJCT: 1094  CCCCTGTTCAGCAGCTCTTCTCCGGGATACCCTTTGACCTCAGGGACCGTTTATACACCA 1153

QUERY: 654   CCGCCCCGCCTGCTGCCCAGGAATACTTTCTCCAGGAAGGCTTTCAAGCTGAAGAAGCCC 713
             || ||||||||||||||  ||||||| |||||||||||||| |||||||||||||| |||
SBJCT: 1154  CCACCCCGCCTGCTGCCACGGAATACATTCTCCAGGAAGGCCTTCAAGCTGAAGAAACCC 1213

QUERY: 714   TCCAAATACTGCAGCTGGAAATGTGCTGCCCTCTCCGCCATTGCCGCGGCCCTCCTCTTG 773
             |||||||||||||| ||||||||||||||||| || ||||| ||||| ||||||||||||
SBJCT: 1214  TCCAAATACTGCAGTTGGAAATGTGCTGCCCTGTCTGCCATCGCCGCCGCCCTCCTCTTG 1273

QUERY: 774   GCTATTTTGCTGGCGTATTTCATAG 798
             || ||||||||||| ||||||||||
SBJCT: 1274  GCCATTTTGCTGGCATATTTCATAG 1298

 SCORE =  480 BITS (242), EXPECT = E-132
 IDENTITIES = 365/406 (89%)
 STRAND = PLUS / PLUS

QUERY: 797   AGTGCCCTGGTCGTTGAAAAACAGCAGCATAGACAGTGGTGAAGCAGAAGTTGGTCGGCG 856
             |||||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||
SBJCT: 1420  AGTGCCCTGGTCATTGAAAAACAGCAGCATAGACAGTGGCGAAGCAGAAGTTGGTCGGCG 1479

QUERY: 857   GGTAACACAAGAAGTCCCACCAGGGGTGTTTTGGAGGTCACAAATTCACATCAGTCAGCC 916
             ||| ||||| ||||||||||||||||||||||||||||| || |||||||||||||||||
SBJCT: 1480  GGTGACACAGGAAGTCCCACCAGGGGTGTTTTGGAGGTCCCAGATTCACATCAGTCAGCC 1539

QUERY: 917   CCAGTTCTTAAAGTTCAACATCTCCCTCGGGAAGGACGCTCTCTTTGGTGTTTACATAAG 976
              || ||||||||||||||||||||||| || ||||| || ||||| ||||| || |||||
SBJCT: 1540  TCAATTCTTAAAGTTCAACATCTCCCTGGGCAAGGATGCCCTCTTCGGTGTCTATATAAG 1599

QUERY: 977   AAGAGGACTTCCACCATCTCATGCCCAGTATGACTTCATGGAACGTCTGGACGGGAAGGA 1036
              |||||||| ||||| ||||||||||||||||||||||||||||| ||||| || |||||
SBJCT: 1600  GAGAGGACTACCACCGTCTCATGCCCAGTATGACTTCATGGAACGCCTGGATGGAAAGGA 1659

QUERY: 1037  GAAGTGGAGTGTGGTTGAGTCTCCCAGGGAACGCCGGAGCATACAGACCTTGGTTCAGAA 1096
             ||| ||||| ||||| ||||| |||||||||||||||||||| |||||  |||| |||||
SBJCT: 1660  GAAATGGAGCGTGGTCGAGTCGCCCAGGGAACGCCGGAGCATCCAGACTCTGGTGCAGAA 1719

QUERY: 1097  TGAAGCCGTGTTTGTGCAGTACCTGGATGTGGGCCTGTGGCATCTGGCCTTCTACAATGA 1156
              || || ||||||||||||||| ||||||||||||||||||| |||||||||||||||||
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```
SBJCT: 1720 CGAGGCTGTGTTTGTGCAGTACTTGGATGTGGGCCTGTGGCACCTGGCCTTCTACAATGA 1779

QUERY: 1157 TGGAAAAGACAAAGAGATGGTTTCCTTCAATACTGTTGTCCTAGAT 1202
             || || ||||| |||||||| |||||||| ||||||||| |||||
SBJCT: 1780 CGGCAAGGACAAGGAGATGGTCTCCTTCAACACTGTTGTCTTAGAT 1825

 SCORE =  125 BITS (63), EXPECT = 7E-26
 IDENTITIES = 93/103 (90%)
 STRAND = PLUS / PLUS

QUERY: 1258 GATTCAGTGCAGGACTGTCCACGTAACTGCCATGGGAATGGTGAATGTGTGTCCGGGGTG 1317
            ||||||||||||||||||||||| ||||| || ||||| |||||||| ||||| ||  ||
SBJCT: 1823 GATTCAGTGCAGGACTGTCCACGGAACTGTCACGGGAACGGTGAATGCGTGTCTGGACTG 1882

QUERY: 1318 TGTCACTGTTTCCCAGGATTTCTAGGAGCAGACTGTGCTAAAG 1360
            |||||||||||||||||||| ||||| ||||||||||||||||
SBJCT: 1883 TGTCACTGTTTCCCAGGATTCCTAGGTGCAGACTGTGCTAAAG 1925
```

In another BLASTN search it was found that the FCTR3a nucleic acid has homology to three fragments of *Gallus gallus* mRNA for teneurin-2. It has 541 of 629 bases (86%) identical to bases 502-1130, 302 of 367 bases (82%) identical to bases 1330-1696, and 87 of 103 bases (84%) identical to bases 1711-1813 of *Gallus gallus* mRNA for teneurin-2 (EMBL Acc: AJ245711.1) (Table 3K).

Table 3K. BLASTN of FCTR3a against *Gallus gallus* mRNA for teneurin-2 (SEQ ID NO:63)

```
>GI|6010048|EMB|AJ245711.1|GGA245711 GALLUS GALLUS MRNA FOR TENEURIN-2, SHORT SPLICE
VARIANT (TEN2 GENE)
          LENGTH = 2496

 SCORE =  549 BITS (277), EXPECT = E-153
 IDENTITIES = 541/629 (86%)
 STRAND = PLUS / PLUS

QUERY: 114  GGTCGTCCCATTCCACCTACATCCTCGCCTAGTCTCCTCCCATCTGCTCAGCTGCCTAGC 173
            ||||||||||||||||||||||||||| |||| || |||||||||||||||||||| || 
SBJCT: 502  GGTCGTCCCATTCCACCTACATCCTCGTCTAGCCTTCTCCCATCTGCTCAGCTGCCCAGT 561

QUERY: 174  TCCCATAATCCTCCACCAGTTAGCTGCCAGATGCCATTGCTAGACAGCAACACCTCCCAT 233
            || ||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
SBJCT: 562  TCTCATAATCCTCCACCAGTTAGCTGCCAGATGCCATTGCTAGACAGCAATACGTCCCAT 621

QUERY: 234  CAAATCATGGACACCAACCCTGATGAGGAATTCTCCCCCAATTCATACCTGCTCAGAGCA 293
            ||||||||||||||||| ||||| ||||| ||||| || ||||||||||| || ||||||
SBJCT: 622  CAAATCATGGACACCAATCCTGACGAGGAGTTCTCTCCTAATTCATACCTACTAAGAGCA 681

QUERY: 294  TGCTCAGGGCCCCAGCAAGCCTCCAGCAGTGGCCCTCCGAACCACCACAGCCAGTCGACT 353
            || |||||||| ||||| || ||||||||||||||| | ||||| ||||||||||| || 
SBJCT: 682  TGTTCAGGGCCACAGCAGGCATCCAGCAGTGGCCCTTCAAACCATCACAGCCAGTCAACG 741

QUERY: 354  CTGAGGCCCCCTCTCCCACCCCCTCACAACCACACGCTGTCCCATCACCACTCGTCCGCC 413
            |||||||| |||||||| || |||||||||||| ||||||||||||| |||||||| |||
SBJCT: 742  CTGAGGCCACCTCTCCCCCCTCCTCACAACCACTCGCTGTCCCATCATCACTCGTCTGCC 801

QUERY: 414  AACTCCCTCAACAGGAACTCACTGACCAATCGGCGGAGTCAGATCCACGCCCCGGCCCCA 473
            |||||||||||||||||||| || ||||| || || |  ||||||||||| || || || 
SBJCT: 802  AACTCCCTCAACAGGAACTCGCTCACCAACCGCCGCAACCAGATCCACGCGCCTGCTCCC 861

QUERY: 474  GCGCCCAATGACCTGGCCACCACACCAGAGTCCGTTCAGCTTCAGGACAGCTGGGTGCTA 533
            || |||||||||||||| ||||| || ||||| || ||||| ||||||||||||||||| 
SBJCT: 862  GCTCCCAATGACCTGGCGACCACGCCTGAGTCTGTGCAGCTGCAGGACAGCTGGGTGCTC 921
```

```
QUERY: 534   AACAGCAACGTGCCACTGGAGACCCGGCACTTCCTCTTCAAGACCTCCTCGGGGAGCACA 593
             |||||||||||||| ||||||||| |||| ||| | || ||||| || || || |  ||
SBJCT: 922   AACAGCAACGTGCCGCTGGAGACCAGGCATTTCTTGTTTAAGACATCTTCTGGAACGACT 981

QUERY: 594   CCCTTGTTCAGCAGCTCTTCCCCGGGATACCCTTTGACCTCAGGAACGGTTTACACGCCC 653
             ||  ||||||| |||||||||||| || |||||  ||||||||||||| ||||| || ||
SBJCT: 982   CCGCTGTTCAGTAGCTCTTCCCCTGGCTACCCACTGACCTCAGGAACAGTTTATACTCCA 1041

QUERY: 654   CCGCCCCGCCTGCTGCCCAGGAATACTTTCTCCAGGAAGGCTTTCAAGCTGAAGAAGCCC 713
             || ||| | ||| | || || ||||| || |||||||| || ||||||||||| ||||||
SBJCT: 1042  CCTCCCAGGCTGTTACCTAGAAATACATTTTCCAGGAATGCATTCAAGCTGAAAAAGCCC 1101

QUERY: 714   TCCAAATACTGCAGCTGGAAATGTGCTGC 742
             ||||| || || ||||||||||||||||
SBJCT: 1102  TCCAAGTATTGTAGCTGGAAATGTGCTGC 1130

 SCORE =  212 BITS (107), EXPECT = 4E-52
 IDENTITIES = 302/367 (82%)
 STRAND = PLUS / PLUS

QUERY: 819   AGCAGCATAGACAGTGGTGAAGCAGAAGTTGGTCGGCGGGTAACACAAGAAGTCCCACCA 878
             ||||||||||| ||||| ||| |||||||||| ||   ||| || ||||| || || ||
SBJCT: 1330  AGCAGCATAGATAGTGGAGAAACAGAAGTTGGCCGCAAGGTCACCCAAGAGGTGCCCCCT 1389

QUERY: 879   GGGGTGTTTTGGAGGTCACAAATTCACATCAGTCAGCCCCAGTTCTTAAAGTTCAACATC 938
             || ||||| ||| |||| || || || ||||| ||||| |||||| | |||||||||||
SBJCT: 1390  GGAGTGTTCTGGCGGTCTCAGATCCATATCAGCCAGCCACAGTTCCTGAAGTTCAACATA 1449

QUERY: 939   TCCCTCGGGAAGGACGCTCTCTTTGGTGTTTACATAAGAAGAGGACTTCCACCATCTCAT 998
             ||||| |||||||| ||||| || |||||||| ||||||||||||| |||||||| |||
SBJCT: 1450  TCCCTAGGGAAGGATGCTCTTTTCGGTGTTTATATAAGAAGAGGACTCCCACCATCACAT 1509

QUERY: 999   GCCCAGTATGACTTCATGGAACGTCTGGACGGGAAGGAGAAGTGGAGTGTGGTTGAGTCT 1058
             || |||||||| |||||||||||  |||| ||||| ||||| ||||||||||| || ||
SBJCT: 1510  GCACAGTATGATTTCATGGAACGCTTGGATGGGAAAGAGAAATGGAGTGTGGTGGAATCC 1569

QUERY: 1059  CCCAGGGAACGCCGGAGCATACAGACCTTGGTTCAGAATGAAGCCGTGTTTGTGCAGTAC 1118
             ||  ||||||| || || || |||||  | ||||||||||| || |||||||| ||||||
SBJCT: 1570  CCACGGGAACGGCGAAGTATTCAGACTCTTGTTCAGAATGAGGCTGTGTTTGTTCAGTAC 1629

QUERY: 1119  CTGGATGTGGGCCTGTGGCATCTGGCCTTCTACAATGATGGAAAAGACAAAGAGATGGTT 1178
              ||||||||||  ||||||| ||||| || |||||||||||| || ||||||||   ||||
SBJCT: 1630  TTGGATGTGGGTTTGTGGCACCTGGCGTTTTACAATGATGGCAAGGACAAAGAAGTGGTC 1689

QUERY: 1179  TCCTTCA 1185
             |||||||
SBJCT: 1690  TCCTTCA 1696

 SCORE = 77.8 BITS (39), EXPECT = 1E-11
 IDENTITIES = 87/103 (84%)
 STRAND = PLUS / PLUS

QUERY: 1258  GATTCAGTGCAGGACTGTCCACGTAACTGCCATGGGAATGGTGAATGTGTGTCCGGGGTG 1317
             ||||||||||| |||||||||||||| || ||||| ||||| || |||||| || || ||
SBJCT: 1711  GATTCAGTGCAAGACTGTCCACGTAATTGTCATGGCAATGGCGAGTGTGTTTCTGGTGTC 1770

QUERY: 1318  TGTCACTGTTTCCCAGGATTTCTAGGAGCAGACTGTGCTAAAG 1360
             || |||||||| || |||||||  |||||||| ||||||||||
SBJCT: 1771  TGCCACTGTTTTCCCGGATTTCATGGAGCAGATTGTGCTAAAG 1813
```

In this search it was also found that the fragments of FCTR3bcd and e nucleic acids had homology to three fragments of *Homo sapiens* mRNA for KIAA1127 protein. It has 5537 of 5538 bases (99%) identical to bases 1-5538, 705 of 714 bases (98%) identical to bases 5609-

6322, and 176 of 176 bases (100%) identical to bases 6385-6560 of *Homo sapiens* mRNA for KIAA1127 protein (GenBank Acc: AB032953) (Table 3L).

Table 3L. BLASTN of FCTR3b, c, d, and e against *Homo sapiens* KIAA1127 mRNA (SEQ ID NO:64)

```
>GI|6329762|DBJ|AB032953.1|AB032953 HOMO SAPIENS MRNA FOR KIAA1127 PROTEIN, PARTIAL
CDS
          LENGTH = 6560

 SCORE = 1.097E+04 BITS (5534), EXPECT = 0.0
 IDENTITIES = 5537/5538 (99%)
 STRAND = PLUS / PLUS

QUERY: 3267 CACCTTCTTTAGTGCTGCCCCTGGGCAGAATCCCATCGTGCCTGAGACCCAGGTTCTTCA 3326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1    CACCTTCTTTAGTGCTGCCCCTGGGCAGAATCCCATCGTGCCTGAGACCCAGGTTCTTCA 60

QUERY: 3327 TGAAGAAATCGAGCTCCCTGGTTCCAATGTGAAACTTCGCTATCTGAGCTCTAGAACTGC 3386
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 61   TGAAGAAATCGAGCTCCCTGGTTCCAATGTGAAACTTCGCTATCTGAGCTCTAGAACTGC 120

QUERY: 3387 AGGGTACAAGTCACTGCTGAAGATCACCATGACCCAGTCCACAGTGCCCCTGAACCTCAT 3446
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 121  AGGGTACAAGTCACTGCTGAAGATCACCATGACCCAGTCCACAGTGCCCCTGAACCTCAT 180

QUERY: 3447 TAGGGTTCACCTGATGGTGGCTGTCGAGGGGCATCTCTTCCAGAAGTCATTCCAGGCTTC 3506
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 181  TAGGGTTCACCTGATGGTGGCTGTCGAGGGGCATCTCTTCCAGAAGTCATTCCAGGCTTC 240

QUERY: 3507 TCCCAACCTGGCCTCCACCTTCATCTGGGACAAGACAGATGCGTATGGCCAAAGGGTGTA 3566
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 241  TCCCAACCTGGCCTACACCTTCATCTGGGACAAGACAGATGCGTATGGCCAAAGGGTGTA 300

QUERY: 3567 TGGACTCTCAGATGCTGTTGTGTCTGTCGGGTTTGAATATGAGACCTGTCCCAGTCTAAT 3626
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 301  TGGACTCTCAGATGCTGTTGTGTCTGTCGGGTTTGAATATGAGACCTGTCCCAGTCTAAT 360

QUERY: 3627 TCTCTGGGAGAAAAGGACAGCCCTCCTTCAGGGATTCGAGCTGGACCCCTCCAACCTCGG 3686
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 361  TCTCTGGGAGAAAAGGACAGCCCTCCTTCAGGGATTCGAGCTGGACCCCTCCAACCTCGG 420

QUERY: 3687 TGGCTGGTCCCTAGACAAACACCACATCCTCAATGTTAAAAGTGGAATCCTACACAAAGG 3746
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 421  TGGCTGGTCCCTAGACAAACACCACATCCTCAATGTTAAAAGTGGAATCCTACACAAAGG 480

QUERY: 3747 CACTGGGGAAAACCAGTTCCTGACCCAGCAGCCTGCCATCATCACCAGCATCATGGGCAA 3806
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 481  CACTGGGGAAAACCAGTTCCTGACCCAGCAGCCTGCCATCATCACCAGCATCATGGGCAA 540

QUERY: 3807 TGGTCGCCGCCGGAGCATTTCCTGTCCCAGCTGCAACGGCCTTGCTGAAGGCAACAAGCT 3866
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 541  TGGTCGCCGCCGGAGCATTTCCTGTCCCAGCTGCAACGGCCTTGCTGAAGGCAACAAGCT 600

QUERY: 3867 GCTGGCCCCAGTGGCTCTGGCTGTTGGAATCGATGGGAGCCTCTATGTGGGTGACTTCAA 3926
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 601  GCTGGCCCCAGTGGCTCTGGCTGTTGGAATCGATGGGAGCCTCTATGTGGGTGACTTCAA 660

QUERY: 3927 TTACATCCGACGCATCTTTCCCTCTCGAAATGTGACCAGCATCTTGGAGTTACGAAATAA 3986
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 661  TTACATCCGACGCATCTTTCCCTCTCGAAATGTGACCAGCATCTTGGAGTTACGAAATAA 720

QUERY: 3987 AGAGTTTAAACATAGCAACAACCCAGCACACAAGTACTACTTGGCAGTGGACCCCGTGTC 4046
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 721  AGAGTTTAAACATAGCAACAACCCAGCACACAAGTACTACTTGGCAGTGGACCCCGTGTC 780

QUERY: 4047 CGGCTCGCTCTACGTGTCCGACACCAACAGCAGGAGAATCTACCGCGTCAAGTCTCTGAG 4106
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 781  CGGCTCGCTCTACGTGTCCGACACCAACAGCAGGAGAATCTACCGCGTCAAGTCTCTGAG 840

QUERY: 4107 TGGAACCAAAGACCTGGCTGGGAATTCGGAAGTTGTGGCAGGGACGGGAGAGCAGTGTCT 4166
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 841  TGGAACCAAAGACCTGGCTGGGAATTCGGAAGTTGTGGCAGGGACGGGAGAGCAGTGTCT 900

QUERY: 4167 ACCCTTTGATGAAGCCCGCTGCGGGGATGGAGGGAAGGCCATAGATGCAACCCTGATGAG 4226
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 901  ACCCTTTGATGAAGCCCGCTGCGGGGATGGAGGGAAGGCCATAGATGCAACCCTGATGAG 960

QUERY: 4227 CCCGAGAGGTATTGCAGTAGACAAGAATGGGCTCATGTACTTTGTCGATGCCACCATGAT 4286
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 961  CCCGAGAGGTATTGCAGTAGACAAGAATGGGCTCATGTACTTTGTCGATGCCACCATGAT 1020

QUERY: 4287 CCGGAAGGTTGACCAGAATGGAATCATCTCCACCCTGCTGGGCTCCAATGACCTCACTGC 4346
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1021 CCGGAAGGTTGACCAGAATGGAATCATCTCCACCCTGCTGGGCTCCAATGACCTCACTGC 1080

QUERY: 4347 CGTCCGGCCGCTGAGCTGTGATTCCAGCATGGATGTAGCCCAGGTTCGTCTGGAGTGGCC 4406
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1081 CGTCCGGCCGCTGAGCTGTGATTCCAGCATGGATGTAGCCCAGGTTCGTCTGGAGTGGCC 1140

QUERY: 4407 AACAGACCTTGCTGTCAATCCCATGGATAACTCCTTGTATGTTCTAGAGAACAATGTCAT 4466
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1141 AACAGACCTTGCTGTCAATCCCATGGATAACTCCTTGTATGTTCTAGAGAACAATGTCAT 1200

QUERY: 4467 CCTTCGAATCACCGAGAACCACCAAGTCAGCATCATTGCGGGACGCCCCATGCACTGCCA 4526
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1201 CCTTCGAATCACCGAGAACCACCAAGTCAGCATCATTGCGGGACGCCCCATGCACTGCCA 1260

QUERY: 4527 AGTTCCTGGCATTGACTACTCACTCAGCAAACTAGCCATTCACTCTGCCCTGGAGTCAGC 4586
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1261 AGTTCCTGGCATTGACTACTCACTCAGCAAACTAGCCATTCACTCTGCCCTGGAGTCAGC 1320

QUERY: 4587 CAGTGCCATTGCCATTTCTCACACTGGGGTCCTCTACATCACTGAGACAGATGAGAAGAA 4646
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1321 CAGTGCCATTGCCATTTCTCACACTGGGGTCCTCTACATCACTGAGACAGATGAGAAGAA 1380

QUERY: 4647 GATTAACCGTCTACGCCAGGTAACAACCAACGGGGAGATCTGCCTTTTAGCTGGGGCAGC 4706
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1381 GATTAACCGTCTACGCCAGGTAACAACCAACGGGGAGATCTGCCTTTTAGCTGGGGCAGC 1440

QUERY: 4707 CTCGGACTGCGACTGCAAAAACGATGTCAATTGCAACTGCTATTCAGGAGATGATGCCTA 4766
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1441 CTCGGACTGCGACTGCAAAAACGATGTCAATTGCAACTGCTATTCAGGAGATGATGCCTA 1500

QUERY: 4767 CGCGACTGATGCCATCTTGAATTCCCCATCATCCTTAGCTGTAGCTCCAGATGGTACCAT 4826
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1501 CGCGACTGATGCCATCTTGAATTCCCCATCATCCTTAGCTGTAGCTCCAGATGGTACCAT 1560

QUERY: 4827 TTACATTGCAGACCTTGGAAATATTCGGATCAGGGCGGTCAGCAAGAACAAGCCTGTTCT 4886
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1561 TTACATTGCAGACCTTGGAAATATTCGGATCAGGGCGGTCAGCAAGAACAAGCCTGTTCT 1620

QUERY: 4887 TAATGCCTTCAACCAGTATGAGGCTGCATCCCCCGGAGAGCAGGAGTTATATGTTTTCAA 4946
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1621 TAATGCCTTCAACCAGTATGAGGCTGCATCCCCCGGAGAGCAGGAGTTATATGTTTTCAA 1680

QUERY: 4947 CGCTGATGGCATCCACCAATACACTGTGAGCCTGGTGACAGGGGAGTACTTGTACAATTT 5006
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1681 CGCTGATGGCATCCACCAATACACTGTGAGCCTGGTGACAGGGGAGTACTTGTACAATTT 1740

QUERY: 5007 CACATATAGTACTGACAATGATGTCACTGAATTGATTGACAATAATGGGAATTCCCTGAA 5066
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1741 CACATATAGTACTGACAATGATGTCACTGAATTGATTGACAATAATGGGAATTCCCTGAA 1800

QUERY: 5067 GATCCGTCGGGACAGCAGTGGCATGCCCCGTCACCTGCTCATGCCTGACAACCAGATCAT 5126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1801 GATCCGTCGGGACAGCAGTGGCATGCCCCGTCACCTGCTCATGCCTGACAACCAGATCAT 1860
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QUERY: 5127 CACCCTCACCGTGGGCACCAATGGAGGCCTCAAAGTCGTGTCCACACAGAACCTGGAGCT 5186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1861 CACCCTCACCGTGGGCACCAATGGAGGCCTCAAAGTCGTGTCCACACAGAACCTGGAGCT 1920

QUERY: 5187 TGGTCTCATGACCTATGATGGCAACACTGGGCTCCTGGCCACCAAGAGCGATGAAACAGG 5246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1921 TGGTCTCATGACCTATGATGGCAACACTGGGCTCCTGGCCACCAAGAGCGATGAAACAGG 1980

QUERY: 5247 ATGGACGACTTTCTATGACTATGACCACGAAGGCCGCCTGACCAACGTGACGCGCCCCAC 5306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1981 ATGGACGACTTTCTATGACTATGACCACGAAGGCCGCCTGACCAACGTGACGCGCCCCAC 2040

QUERY: 5307 GGGGGTGGTAACCAGTCTGCACCGGGAAATGGAGAAATCTATTACCATTGACATTGAGAA 5366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2041 GGGGGTGGTAACCAGTCTGCACCGGGAAATGGAGAAATCTATTACCATTGACATTGAGAA 2100

QUERY: 5367 CTCCAACCGTGATGATGACGTCACTGTCATCACCAACCTCTCTTCAGTAGAGGCCTCCTA 5426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2101 CTCCAACCGTGATGATGACGTCACTGTCATCACCAACCTCTCTTCAGTAGAGGCCTCCTA 2160

QUERY: 5427 CACAGTGGTACAAGATCAAGTTCGGAACAGCTACCAGCTCTGTAATAATGGTACCCTGAG 5486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2161 CACAGTGGTACAAGATCAAGTTCGGAACAGCTACCAGCTCTGTAATAATGGTACCCTGAG 2220

QUERY: 5487 GGTGATGTATGCTAATGGGATGGGTATCAGCTTCCACAGCGAGCCCCATGTCCTAGCGGG 5546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2221 GGTGATGTATGCTAATGGGATGGGTATCAGCTTCCACAGCGAGCCCCATGTCCTAGCGGG 2280

QUERY: 5547 CACCATCACCCCCACCATTGGACGCTGCAACATCTCCCTGCCTATGGAGAATGGCTTAAA 5606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2281 CACCATCACCCCCACCATTGGACGCTGCAACATCTCCCTGCCTATGGAGAATGGCTTAAA 2340

QUERY: 5607 CTCCATTGAGTGGCGCCTAAGAAAGGAACAGATTAAAGGCAAAGTCACCATCTTTGGCAG 5666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2341 CTCCATTGAGTGGCGCCTAAGAAAGGAACAGATTAAAGGCAAAGTCACCATCTTTGGCAG 2400

QUERY: 5667 GAAGCTCCGGGTCCATGGAAGAAATCTCTTGTCCATTGACTATGATCGAAATATTCGGAC 5726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2401 GAAGCTCCGGGTCCATGGAAGAAATCTCTTGTCCATTGACTATGATCGAAATATTCGGAC 2460

QUERY: 5727 TGAAAAGATCTATGATGACCACCGGAAGTTCACCCTGAGGATCATTTATGACCAGGTGGG 5786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2461 TGAAAAGATCTATGATGACCACCGGAAGTTCACCCTGAGGATCATTTATGACCAGGTGGG 2520

QUERY: 5787 CCGCCCCTTCCTCTGGCTGCCCAGCAGCGGGCTGGCAGCTGTCAACGTGTCATACTTCTT 5846
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2521 CCGCCCCTTCCTCTGGCTGCCCAGCAGCGGGCTGGCAGCTGTCAACGTGTCATACTTCTT 2580

QUERY: 5847 CAATGGGCGCCTGGCTGGGCTTCAGCGTGGGGCCATGAGCGAGAGGACAGACATCGACAA 5906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2581 CAATGGGCGCCTGGCTGGGCTTCAGCGTGGGGCCATGAGCGAGAGGACAGACATCGACAA 2640

QUERY: 5907 GCAAGGCCGCATCGTGTCCCGCATGTTCGCTGACGGGAAAGTGTGGAGCTACTCCTACCT 5966
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2641 GCAAGGCCGCATCGTGTCCCGCATGTTCGCTGACGGGAAAGTGTGGAGCTACTCCTACCT 2700

QUERY: 5967 TGACAAGTCCATGGTCCTCCTGCTTCAGAGCCAACGTCAGTATATATTTGAGTATGACTC 6026
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2701 TGACAAGTCCATGGTCCTCCTGCTTCAGAGCCAACGTCAGTATATATTTGAGTATGACTC 2760

QUERY: 6027 CTCTGACCGCCTCCTTGCCGTCACCATGCCCAGCGTGGCCCGGCACAGCATGTCCACACA 6086
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2761 CTCTGACCGCCTCCTTGCCGTCACCATGCCCAGCGTGGCCCGGCACAGCATGTCCACACA 2820

QUERY: 6087 CACCTCCATCGGCTACATCCGTAATATTTACAACCCGCCTGAAAGCAATGCTTCGGTCAT 6146
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2821 CACCTCCATCGGCTACATCCGTAATATTTACAACCCGCCTGAAAGCAATGCTTCGGTCAT 2880

QUERY: 6147 CTTTGACTACAGTGATGACGGCCGCATCCTGAAGACCTCCTTTTTGGGCACCGGACGCCA 6206
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2881 CTTTGACTACAGTGATGACGGCCGCATCCTGAAGACCTCCTTTTTGGCACCGGACGCCA 2940

QUERY: 6207 GGTGTTCTACAAGTATGGGAAACTCTCCAAGTTATCAGAGATTGTCTACGACAGTACCGC 6266
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2941 GGTGTTCTACAAGTATGGGAAACTCTCCAAGTTATCAGAGATTGTCTACGACAGTACCGC 3000

QUERY: 6267 CGTCACCTTCGGGTATGACGAGACCACTGGTGTCTTGAAGATGGTCAACCTCCAAAGTGG 6326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3001 CGTCACCTTCGGGTATGACGAGACCACTGGTGTCTTGAAGATGGTCAACCTCCAAAGTGG 3060

QUERY: 6327 GGCTTCTCCTGCACCATCAGGTACCGGAAGATTGGCCCCCTGGTGGACAAGCAGATCTA 6386
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3061 GGCTTCTCCTGCACCATCAGGTACCGGAAGATTGGCCCCCTGGTGGACAAGCAGATCTA 3120

QUERY: 6387 CAGGTTCTCCGAGGAAGGCATGGTCAATGCCAGGTTTGACTACACCTATCATGACAACAG 6446
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3121 CAGGTTCTCCGAGGAAGGCATGGTCAATGCCAGGTTTGACTACACCTATCATGACAACAG 3180

QUERY: 6447 CTTCCGCATCGCAAGCATCAAGCCCGTCATAAGTGAGACTCCCCTCCCCGTTGACCTCTA 6506
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3181 CTTCCGCATCGCAAGCATCAAGCCCGTCATAAGTGAGACTCCCCTCCCCGTTGACCTCTA 3240

QUERY: 6507 CCGCTATGATGAGATTTCTGGCAAGGTGGAACACTTTGGTAAGTTTGGAGTCATCTATTA 6566
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3241 CCGCTATGATGAGATTTCTGGCAAGGTGGAACACTTTGGTAAGTTTGGAGTCATCTATTA 3300

QUERY: 6567 TGACATCAACCAGATCATCACCACTGCCGTGATGACCCTCAGCAAACACTTCGACACCCA 6626
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3301 TGACATCAACCAGATCATCACCACTGCCGTGATGACCCTCAGCAAACACTTCGACACCCA 3360

QUERY: 6627 TGGGCGGATCAAGGAGGTCCAGTATGAGATGTTCCGGTCCCTCATGTACTGGATGACGGT 6686
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3361 TGGGCGGATCAAGGAGGTCCAGTATGAGATGTTCCGGTCCCTCATGTACTGGATGACGGT 3420

QUERY: 6687 GCAATATGACAGCATGGGCAGGGTGATCAAGAGGGAGCTAAAACTGGGGCCCTATGCCAA 6746
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3421 GCAATATGACAGCATGGGCAGGGTGATCAAGAGGGAGCTAAAACTGGGGCCCTATGCCAA 3480

QUERY: 6747 TACCACGAAGTACACCTATGACTACGATGGGGACGGGCAGCTCCAGAGCGTGGCCGTCAA 6806
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3481 TACCACGAAGTACACCTATGACTACGATGGGGACGGGCAGCTCCAGAGCGTGGCCGTCAA 3540

QUERY: 6807 TGACCGCCCGACCTGGCGCTACAGCTATGACCTTAATGGGAATCTCCACTTACTGAACCC 6866
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3541 TGACCGCCCGACCTGGCGCTACAGCTATGACCTTAATGGGAATCTCCACTTACTGAACCC 3600

QUERY: 6867 AGGCAACAGTGTGCGCCTCATGCCCTTGCGCTATGACCTCCGGGATCGGATAACCAGACT 6926
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3601 AGGCAACAGTGTGCGCCTCATGCCCTTGCGCTATGACCTCCGGGATCGGATAACCAGACT 3660

QUERY: 6927 CGGGGATGTGCAGTACAAAATTGACGACGATGGCTATCTGTGCCAGAGAGGGTCTGACAT 6986
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3661 CGGGGATGTGCAGTACAAAATTGACGACGATGGCTATCTGTGCCAGAGAGGGTCTGACAT 3720

QUERY: 6987 CTTCGAATACAATTCCAAGGGCCTCCTAACAAGAGCCTACAACAAGGCCAGCGGGTGGAG 7046
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3721 CTTCGAATACAATTCCAAGGGCCTCCTAACAAGAGCCTACAACAAGGCCAGCGGGTGGAG 3780

QUERY: 7047 TGTCCAGTACCGCTATGATGGCGTAGGACGGCGGGCTTCCTACAAGACCAACCTGGGCCA 7106
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3781 TGTCCAGTACCGCTATGATGGCGTAGGACGGCGGGCTTCCTACAAGACCAACCTGGGCCA 3840

QUERY: 7107 CCACCTGCAGTACTTCTACTCTGACCTCCACAACCCGACGCGCATCACCCATGTCTACAA 7166
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3841 CCACCTGCAGTACTTCTACTCTGACCTCCACAACCCGACGCGCATCACCCATGTCTACAA 3900

QUERY: 7167 TCACTCCAACTCGGAGATTACCTCACTGTACTACGACCTCCAGGGCCACCTCTTTGCCAT 7226
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3901 TCACTCCAACTCGGAGATTACCTCACTGTACTACGACCTCCAGGGCCACCTCTTTGCCAT 3960
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QUERY: 7227 GGAGAGCAGCAGTGGGGAGGAGTACTATGTTGCCTCTGATAACACAGGGACTCCTCTGGC 7286
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3961 GGAGAGCAGCAGTGGGGAGGAGTACTATGTTGCCTCTGATAACACAGGGACTCCTCTGGC 4020

QUERY: 7287 TGTGTTCAGCATCAACGGCCTCATGATCAAACAGCTGCAGTACACGGCCTATGGGGAGAT 7346
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4021 TGTGTTCAGCATCAACGGCCTCATGATCAAACAGCTGCAGTACACGGCCTATGGGGAGAT 4080

QUERY: 7347 TTATTATGACTCCAACCCCGACTTCCAGATGGTCATTGGCTTCCATGGGGGACTCTATGA 7406
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4081 TTATTATGACTCCAACCCCGACTTCCAGATGGTCATTGGCTTCCATGGGGGACTCTATGA 4140

QUERY: 7407 CCCCCTGACCAAGCTGGTCCACTTCACTCAGCGTGATTATGATGTGCTGGCAGGACGATG 7466
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4141 CCCCCTGACCAAGCTGGTCCACTTCACTCAGCGTGATTATGATGTGCTGGCAGGACGATG 4200

QUERY: 7467 GACCTCCCCAGACTATACCATGTGGAAAAACGTGGGCAAGGAGCCGGCCCCCTTTAACCT 7526
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4201 GACCTCCCCAGACTATACCATGTGGAAAAACGTGGGCAAGGAGCCGGCCCCCTTTAACCT 4260

QUERY: 7527 GTATATGTTCAAGAGCAACAATCCTCTCAGCAGTGAGCTAGATTTGAAGAACTACGTGAC 7586
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4261 GTATATGTTCAAGAGCAACAATCCTCTCAGCAGTGAGCTAGATTTGAAGAACTACGTGAC 4320

QUERY: 7587 AGATGTGAAAAGCTGGCTTGTGATGTTTGGATTTCAGCTTAGCAACATCATTCCTGGCTT 7646
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4321 AGATGTGAAAAGCTGGCTTGTGATGTTTGGATTTCAGCTTAGCAACATCATTCCTGGCTT 4380

QUERY: 7647 CCCGAGAGCCAAAATGTATTTCGTGCCTCCTCCCTATGAATTGTCAGAGAGTCAAGCAAG 7706
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4381 CCCGAGAGCCAAAATGTATTTCGTGCCTCCTCCCTATGAATTGTCAGAGAGTCAAGCAAG 4440

QUERY: 7707 TGAGAATGGACAGCTCATTACAGGTGTCCAACAGACAACAGAGAGACATAACCAGGCCTT 7766
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4441 TGAGAATGGACAGCTCATTACAGGTGTCCAACAGACAACAGAGAGACATAACCAGGCCTT 4500

QUERY: 7767 CATGGCTCTGGAAGGACAGGTCATTACTAAAAAGCTCCACGCCAGCATCCGAGAGAAAGC 7826
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4501 CATGGCTCTGGAAGGACAGGTCATTACTAAAAAGCTCCACGCCAGCATCCGAGAGAAAGC 4560

QUERY: 7827 AGGTCACTGGTTTGCCACCACCACGCCCATCATTGGCAAAGGCATCATGTTTGCCATCAA 7886
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4561 AGGTCACTGGTTTGCCACCACCACGCCCATCATTGGCAAAGGCATCATGTTTGCCATCAA 4620

QUERY: 7887 AGAAGGGCGGGTGACCACGGGCGTGTCCAGCATCGCCAGCGAAGATAGCCGCAAGGTGGC 7946
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4621 AGAAGGGCGGGTGACCACGGGCGTGTCCAGCATCGCCAGCGAAGATAGCCGCAAGGTGGC 4680

QUERY: 7947 ATCTGTGCTGAACAACGCCTACTACCTGGACAAGATGCACTACAGCATCGAGGGCAAGGA 8006
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4681 ATCTGTGCTGAACAACGCCTACTACCTGGACAAGATGCACTACAGCATCGAGGGCAAGGA 4740

QUERY: 8007 CACCCACTACTTTGTGAAGATTGGCTCAGCCGATGGCGACCTGGTCACACTAGGCACCAC 8066
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4741 CACCCACTACTTTGTGAAGATTGGCTCAGCCGATGGCGACCTGGTCACACTAGGCACCAC 4800

QUERY: 8067 CATCGGCCGCAAGGTGCTAGAGAGCGGGGTGAACGTGACCGTGTCCCAGCCCACGCTGCT 8126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4801 CATCGGCCGCAAGGTGCTAGAGAGCGGGGTGAACGTGACCGTGTCCCAGCCCACGCTGCT 4860

QUERY: 8127 GGTCAACGGCAGGACTCGAAGGTTCACGAACATTGAGTTCCAGTACTCCACGCTGCTGCT 8186
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4861 GGTCAACGGCAGGACTCGAAGGTTCACGAACATTGAGTTCCAGTACTCCACGCTGCTGCT 4920

QUERY: 8187 CAGCATCCGCTATGGCCTCACCCCCGACACCCTGGACGAAGAGAAGGCCCCGCGTCCTGGA 8246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4921 CAGCATCCGCTATGGCCTCACCCCCGACACCCTGGACGAAGAGAAGGCCCCGCGTCCTGGA 4980

QUERY: 8247 CCAGGCGAGACAGAGGGCCCTGGGCACGGCCTGGGCCAAGGAGCAGCAGAAAGCCAGGGA 8306
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                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 4981 CCAGGCGAGACAGAGGGCCCTGGGCACGGCCTGGGCCAAGGAGCAGCAGAAAGCCAGGGA 5040

QUERY: 8307 CGGGAGAGAGGGGAGCCGCCTGTGGACTGAGGGCGAGAAGCAGCAGCTTCTGAGCACCGG 8366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5041 CGGGAGAGAGGGGAGCCGCCTGTGGACTGAGGGCGAGAAGCAGCAGCTTCTGAGCACCGG 5100

QUERY: 8367 GCGCGTGCAAGGGTACGAGGGATATTACGTGCTTCCCGTGGAGCAATACCCAGAGCTTGC 8426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5101 GCGCGTGCAAGGGTACGAGGGATATTACGTGCTTCCCGTGGAGCAATACCCAGAGCTTGC 5160

QUERY: 8427 AGACAGTAGCAGCAACATCCAGTTTTTAAGACAGAATGAGATGGAAAGAGGTAACAAAA 8486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5161 AGACAGTAGCAGCAACATCCAGTTTTTAAGACAGAATGAGATGGAAAGAGGTAACAAAA 5220

QUERY: 8487 TAATCTGCTGCCATTCCTTGTCTGAATGGCTCAGCAGGAGTAACTGTTATCTCCTCTCCT 8546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5221 TAATCTGCTGCCATTCCTTGTCTGAATGGCTCAGCAGGAGTAACTGTTATCTCCTCTCCT 5280

QUERY: 8547 AAGGAGATGAAGACCTAACAGGGGCACTGCGGCTGGGCTGCTTTAGGAGACCAAGTGGCA 8606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5281 AAGGAGATGAAGACCTAACAGGGGCACTGCGGCTGGGCTGCTTTAGGAGACCAAGTGGCA 5340

QUERY: 8607 AGAAAGCTCACATTTTTTGAGTTCAAATGCTACTGTCCAAGCGAGAAGTCCCTCATCCTG 8666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5341 AGAAAGCTCACATTTTTTGAGTTCAAATGCTACTGTCCAAGCGAGAAGTCCCTCATCCTG 5400

QUERY: 8667 AAGTAGACTAAAGCCCGGCTGAAAATTCCGAGGAAAACAAAACAAACGAATGAATGAACA 8726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5401 AAGTAGACTAAAGCCCGGCTGAAAATTCCGAGGAAAACAAAACAAACGAATGAATGAACA 5460

QUERY: 8727 GACACACACAATGTTCCAAGTTCCCCTAAAATATGACCCACTTGTTCTGGGTCTACGCAG 8786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5461 GACACACACAATGTTCCAAGTTCCCCTAAAATATGACCCACTTGTTCTGGGTCTACGCAG 5520

QUERY: 8787 AAAAGAGACGCAAAGTGT 8804
            ||||||||||||||||||
SBJCT: 5521 AAAAGAGACGCAAAGTGT 5538

SCORE = 1362 BITS (687), EXPECT = 0.0
 IDENTITIES = 705/714 (98%)
 STRAND = PLUS / PLUS

QUERY: 8875 CACGGACCGATAAACAAAGAAGCGAAGATAAGAAAGAAGGCCTCATATCCAATTACCTCA 8934
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5609 CACGGACCGATAAACAAAGAAGCGAAGATAAGAAAGAAGGCCTCATATCCAATTACCTCA 5668

QUERY: 8935 CTCATTCACATGTGAGCGACACGCAGACATCCGCGAGGGCCAGCGTCACCAGACCAGCTG 8994
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5669 CTCATTCACATGTGAGCGACACGCAGACATCCGCGAGGGCCAGCGTCACCAGACCAGCTG 5728

QUERY: 8995 CGGGACAAACCACTCAGACTGCTTGTAGGACAAATACTTCTGACATTTTCGTTTAAGCAA 9054
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5729 CGGGACAAACCACTCAGACTGCTTGTAGGACAAATACTTCTGACATTTTCGTTTAAGCAA 5788

QUERY: 9055 ATACAGGTGCATTTAAAACACGACTTTGGGGGTGATTTGTGTGTAGCGCCTGGGGAGGGG 9114
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5789 ATACAGGTGCATTTAAAACACGACTTTGGGGGTGATTTGTGTGTAGCGCCTGGGGAGGGG 5848

QUERY: 9115 GGATAAAAGAGGAGGAGTGAGCACTGGAAATACTTTTTAAAGNNNNNNNNNCATGAGGGA 9174
            ||||||||||||||||||||||||||||||||||||||||||         |||||||||
SBJCT: 5849 GGATAAAAGAGGAGGAGTGAGCACTGGAAATACTTTTTAAAGAAAAAAAAACATGAGGGA 5908

QUERY: 9175 ATAAAAGAAATTCCTATCAAAAATCAAAGTGAAATAATACCATCCAGCACTTAACTCTCA 9234
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5909 ATAAAAGAAATTCCTATCAAAAATCAAAGTGAAATAATACCATCCAGCACTTAACTCTCA 5968

QUERY: 9235 GGTCCCAACTAAGTCTGGCCTGAGCTAATTTATTTGAGCGCAGAGTGTAAAATTTAATTC 9294
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 5969 GGTCCCAACTAAGTCTGGCCTGAGCTAATTTATTTGAGCGCAGAGTGTAAAATTTAATTC 6028
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QUERY: 9295 AAAATGGTGGCTATAATCACTACAGATAAATTTCATACTCTTTTGTCTTTGGAGATTCCA 9354
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 6029 AAAATGGTGGCTATAATCACTACAGATAAATTTCATACTCTTTTGTCTTTGGAGATTCCA 6088

QUERY: 9355 TTGTGGACAGTAATACGCAGTTACAGGGTGTAGTCTGTTTAGATTCCGTAGTTCGTGGGT 9414
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 6089 TTGTGGACAGTAATACGCAGTTACAGGGTGTAGTCTGTTTAGATTCCGTAGTTCGTGGGT 6148

QUERY: 9415 ATCAGTTTCGGTAGAGGTGCAGCATCGTGACACTTTTGCTAACAGGTACCACTTCTGATC 9474
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 6149 ATCAGTTTCGGTAGAGGTGCAGCATCGTGACACTTTTGCTAACAGGTACCACTTCTGATC 6208

QUERY: 9475 ACCCTGTACATACATGAGCCGAAAGGCACAATCACTGTTTCAGATTTAAAATTATTAGTG 9534
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 6209 ACCCTGTACATACATGAGCCGAAAGGCACAATCACTGTTTCAGATTTAAAATTATTAGTG 6268

QUERY: 9535 TGTTTGTTTGGTCCAGAAACTGAGACAATCACATGACAGTCACCACGAGGAGAG 9588
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 6269 TGTTTGTTTGGTCCAGAAACTGAGACAATCACATGACAGTCACCACGAGGAGAG 6322

SCORE =  349 BITS (176), EXPECT = 2E-92
 IDENTITIES = 176/176 (100%)
 STRAND = PLUS / PLUS

QUERY: 9651 GTCTAATAAGAACTTTGGTACAGGAACTTTTTTGTAATATACATGTATGAATTGTTCATC 9710
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 6385 GTCTAATAAGAACTTTGGTACAGGAACTTTTTTGTAATATACATGTATGAATTGTTCATC 6444

QUERY: 9711 GAGTTTTTATATTAATTTTAATTTGCTGCTAAGCAAAGACTAGGGACAGGCAAAGATAAT 9770
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 6445 GAGTTTTTATATTAATTTTAATTTGCTGCTAAGCAAAGACTAGGGACAGGCAAAGATAAT 6504

QUERY: 9771 TTATGGCAAAGTGTTTAAATTGTTTATACATAAATAAAGTCTCTAAAACTCCTGTG 9826
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 6505 TTATGGCAAAGTGTTTAAATTGTTTATACATAAATAAAGTCTCTAAAACTCCTGTG 6560
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In this search it was also found that the FCTR3bcd and e nucleic acids had homology to five fragments of *Mus musculus* mRNA for Ten-m2. It has 5498 of 6108 bases (90%) identical to bases 2504-8610, 1095 of 1196 bases (91%) identical to bases 103-1298, 1000 of 1088 bases (91%) identical to bases 1420-2540, 81 of 89 bases (91%) identical to bases 8655-8743, and 30 of 32 bases (93%) identical to bases 7-38 of *Mus musculus* mRNA for Ten-m2 (Table 3M).

Table 3M. BLASTN of FCTR3b, c, d, and e against *Mus musculus* mRNA for Ten-m2 Mrna (SEQ ID NO:65)

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>GI|4760777|DBJ|AB025411.1|AB025411 MUS MUSCULUS MRNA FOR TEN-M2, COMPLETE CDS
          LENGTH = 8797

 SCORE = 7263 BITS (3664), EXPECT = 0.0
 IDENTITIES = 5498/6108 (90%), GAPS = 1/6108 (0%)
 STRAND = PLUS / PLUS

QUERY: 2578 GATGGCTGCCCTGACTTGTGCAACGGTAACGGGAGATGCACACTGGGTCAGAACAGCTGG 2637
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2504 GATGGCTGCCCTGATTTGTGCAACGGTAACGGGAGATGCACACTGGGTCAGAACAGCTGG 2563

QUERY: 2638 CAGTGTGTCTGCCAGACCGGCTGGAGAGGGCCCGGATGCAACGTTGCCATGGAAACTTCC 2697
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||| |||
SBJCT: 2564 CAGTGTGTCTGCCAGACCGGCTGGAGAGGGCCTGGATGCAACGTTGCCATGGAAACCTCC 2623

QUERY: 2698 TGTGCTGATAACAAGGATAATGAGGGAGATGGCCTGGTGGATTGTTTGGACCCTGACTGC 2757
            || |||||||||||||||||||||||||||||||||||||| ||  ||||||||||||||
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SBJCT: 2624 TGCGCTGATAACAAGGATAATGAGGGAGATGGCCTGGTGGACTGCCTGGACCCTGACTGC 2683

QUERY: 2758 TGCCTGCAGTCAGCCTGTCAGAACAGCCTGCTCTGCCGGGGGTCCCGGGACCCACTGGAC 2817
            ||||| |||||||||||||||||||||||||||||||||||||| ||||||||  |||||
SBJCT: 2684 TGCCTACAGTCAGCCTGTCAGAACAGCCTGCTCTGCCGGGGGTCTCGGGACCCCTTGGAC 2743

QUERY: 2818 ATCATTCAGCAGGGCCAGACGGATTGGCCCGCAGTGAAGTCCTTCTATGACCGTATCAAG 2877
            ||||||||||| || ||||| || ||||| ||||||||||||||||||||||| ||||||
SBJCT: 2744 ATCATTCAGCAAGGTCAGACAGACTGGCCTGCAGTGAAGTCCTTCTATGACCGCATCAAG 2803

QUERY: 2878 CTCTTGGCAGGCAAGGATAGCACCCACATCATTCCTGGAGAGAACCCTTTCAACAGCAGC 2937
            ||||||||||||||||| ||||||||||||||||||||||| ||||| ||||| ||||||
SBJCT: 2804 CTCTTGGCAGGCAAGGACAGCACCCACATCATTCCTGGAGACAACCCCTTCAATAGCAGC 2863

QUERY: 2938 TTGGTTTCTCTCATCCGAGGCCAAGTAGTAACTACAGATGGAACTCCCCTGGTCGGTGTG 2997
             |||| ||||| |||||||||||||||||||| |  ||||| |||||| |||| ||||||
SBJCT: 2864 CTGGTGTCTCTGATCCGAGGCCAAGTAGTAACCATGGATGGGACTCCCTTGGTGGGTGTG 2923

QUERY: 2998 AACGTGTCTTTTGTCAAGTACCCAAAATACGGCTACACCATCACCCGCCAGGATGGCACG 3057
            || |||||||||||||||||||||||||| |||||||||||||| |||||||||||||||
SBJCT: 2924 AATGTGTCTTTTGTCAAGTACCCAAAATATGGCTACACCATCACTCGCCAGGATGGCACG 2983

QUERY: 3058 TTCGACCTGATCGCAAATGGAGGTGCTTCCTTGACTCTACACTTTGAGCGAGCCCCGTTC 3117
            || |||||||| || ||||| ||| || |||||||||| ||||||||||||||||| |||
SBJCT: 2984 TTTGACCTGATTGCCAATGGGGGTTCTGCCTTGACTCTTCACTTTGAGCGAGCCCCTTTC 3043

QUERY: 3118 ATGAGCCAGGAGCGCACTGTGTGGCTGCCGTGGAACAGCTTTTACGCCATGGACACCCTG 3177
            ||||||||||||||||| ||||||||||| ||||||||||| || |||||||||||||||
SBJCT: 3044 ATGAGCCAGGAGCGCACAGTGTGGCTGCCATGGAACAGCTTCTATGCCATGGACACCCTG 3103

QUERY: 3178 GTGATGAAGACCGAGGAGAACTCCATCCCCAGCTGTGACCTCAGTGGCTTTGTCCGGCCT 3237
            || |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
SBJCT: 3104 GTAATGAAGACCGAGGAAAACTCCATCCCCAGCTGTGACCTCAGTGGCTTTGTCCGGCCA 3163

QUERY: 3238 GATCCAATCATCATCTCCTCCCCACTGTCCACCTTCTTTAGTGCTGCCCCTGGGCAGAAT 3297
            |||||||||||||||||||| || |||||||||||||| || ||| ||||||    |||
SBJCT: 3164 GATCCAATCATCATCTCCTCTCCTCTGTCCACCTTCTTCAGCGCTTCCCCTGCCTCGAAC 3223

QUERY: 3298 CCCATCGTGCCTGAGACCCAGGTTCTTCATGAAGAAATCGAGCTCCCTGGTTCCAATGTG 3357
            ||||| |||||||||||||||||||||||||||||||| |||||||||||| ||||||||
SBJCT: 3224 CCCATTGTGCCTGAGACCCAGGTTCTTCATGAAGAAATTGAGCTCCCTGGTACCAATGTG 3283

QUERY: 3358 AAACTTCGCTATCTGAGCTCTAGAACTGCAGGGTACAAGTCACTGCTGAAGATCACCATG 3417
            || || || ||||| |||||||||||||||||||| ||||| ||||||||||||||||||
SBJCT: 3284 AAGCTCCGTTATCTCAGCTCTAGAACTGCAGGGTATAAGTCGCTGCTGAAGATCACCATG 3343

QUERY: 3418 ACCCAGTCCACAGTGCCCCTGAACCTCATTAGGGTTCACCTGATGGTGGCTGTCGAGGGG 3477
            || ||||||||||||||| |||||||||| ||||||||| ||||||| ||||| ||||||
SBJCT: 3344 ACGCAGTCCACAGTGCCCTTGAACCTCATCAGGGTTCACTTGATGGTTGCTGTAGAGGGG 3403

QUERY: 3478 CATCTCTTCCAGAAGTCATTCCAGGCTTCTCCCAACCTGGCCTCCACCTTCATCTGGGAC 3537
            |||||||||||||||||||||||||||||||||||||| |||| ||| ||||||||||||
SBJCT: 3404 CATCTCTTCCAGAAGTCATTCCAGGCTTCTCCCAACCTAGCCTACACATTCATCTGGGAC 3463

QUERY: 3538 AAGACAGATGCGTATGGCCAAAGGGTGTATGGACTCTCAGATGCTGTTGTGTCTGTCGGG 3597
            ||||||||||| |||||||||||||| ||||| || || ||||||||||||||||| |||
SBJCT: 3464 AAGACAGATGCTTATGGCCAAAGGGTTTATGGCCTATCGGATGCTGTTGTGTCTGTTGGG 3523

QUERY: 3598 TTTGAATATGAGACCTGTCCCAGTCTAATTCTCTGGGAGAAAAGGACAGCCCTCCTTCAG 3657
            ||||||||||||||||| |||||||| || || |||||||||||||||||||| ||||||
SBJCT: 3524 TTTGAATATGAGACCTGCCCCAGTCTCATCCTGTGGGAGAAAAGGACAGCCCTGCTTCAG 3583

QUERY: 3658 GGATTCGAGCTGGACCCCTCCAACCTCGGTGGCTGGTCCCTAGACAAACACCACATCCTC 3717
            ||||||||||||||||| |||||||| || ||||||||||| ||||||||||||| ||||
SBJCT: 3584 GGATTCGAGCTGGACCCTTCCAACCTTGGAGGCTGGTCCCTGGACAAACACCACACCCTC 3643

QUERY: 3718 AATGTTAAAAGTGGAATCCTACACAAAGGCACTGGGGAAAACCAGTTCCTGACCCAGCAG 3777
            ||||| ||||| ||||| ||||||||||| || ||||| |||||||||||||||||||||
SBJCT: 3644 AATGTGAAAAGCGGAATACTACACAAAGGGACAGGGGAGAACCAGTTCCTGACCCAGCAG 3703
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QUERY: 3778 CCTGCCATCATCACCAGCATCATGGGCAATGGTCGCCGCCGGAGCATTTCCTGTCCCAGC 3837
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SBJCT: 3704 CCTGCCATCATCACGAGCATCATGGGCAACGGTCGCCGCAGAAGCATCTCCTGTCCCAGC 3763

QUERY: 3838 TGCAACGGCCTTGCTGAAGGCAACAAGCTGCTGGCCCCAGTGGCTCTGGCTGTTGGAATC 3897
            ||||| |||||||||||||||||||| ||| | ||||| ||||| |||||||| || |||
SBJCT: 3764 TGCAATGGCCTTGCTGAAGGCAACAAACTGTTAGCCCCTGTGGCCCTGGCTGTGGGGATC 3823

QUERY: 3898 GATGGGAGCCTCTATGTGGGTGACTTCAATTACATCCGACGCATCTTTCCCTCTCGAAAT 3957
            ||||||||||||| ||| ||||||||||| || ||||| |||||||||||||||||||||
SBJCT: 3824 GATGGGAGCCTCTTTGTTGGTGACTTCAACTATATCCGGCGCATCTTTCCCTCTCGAAAT 3883

QUERY: 3958 GTGACCAGCATCTTGGAGTTACGAAATAAAGAGTTTAAACATAGCAACAACCCAGCACAC 4017
            |||||||| |||||||||||||||||||||||||||||||||||||||| ||||| ||||
SBJCT: 3884 GTGACCAGTATCTTGGAGTTACGAAATAAAGAGTTTAAACATAGCAACAGCCCAGGACAC 3943

QUERY: 4018 AAGTACTACTTGGCAGTGGACCCCGTGTCCGGCTCGCTCTACGTGTCCGACACCAACAGC 4077
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SBJCT: 3944 AAGTACTACTTGGCTGTGGACCCCGTGACTGGCTCACTCTACGTCTCTGACACCAACAGT 4003

QUERY: 4078 AGGAGAATCTACCGCGTCAAGTCTCTGAGTGGAACCAAAGACCTGGCTGGGAATTCGGAA 4137
             |  |||||||||| |||||||||||||| ||| |||||||||||||||| |||||||||
SBJCT: 4004 CGCCGAATCTACCGAGTCAAGTCTCTGAGCGGAGCCAAAGACCTGGCTGGAAATTCGGAA 4063

QUERY: 4138 GTTGTGGCAGGGACGGGAGAGCAGTGTCTACCCTTTGATGAAGCCCGCTGCGGGGATGGA 4197
            |||||||||||||| || || || |||||||||||||||||||||||||| |||||||||
SBJCT: 4064 GTTGTGGCAGGGACTGGCGAACAATGTCTACCCTTTGATGAAGCCCGCTGTGGGGATGGA 4123

QUERY: 4198 GGGAAGGCCATAGATGCAACCCTGATGAGCCCGAGAGGTATTGCAGTAGACAAGAATGGG 4257
            ||||||||  | || || |||||||||||||| |||||||||||||||||||||||||||
SBJCT: 4124 GGGAAGGCTGTGGACGCCACCCTGATGAGCCCCAGAGGTATTGCAGTAGACAAGAATGGG 4183

QUERY: 4258 CTCATGTACTTTGTCGATGCCACCATGATCCGGAAGGTTGACCAGAATGGAATCATCTCC 4317
            || ||||||||||| ||||||||||||||||||||||| ||||| || ||||||||||||
SBJCT: 4184 CTTATGTACTTTGTTGATGCCACCATGATCCGGAAGGTGGACCAAAACGGAATCATCTCC 4243

QUERY: 4318 ACCCTGCTGGGCTCCAATGACCTCACTGCCGTCCGGCCGCTGAGCTGTGATTCCAGCATG 4377
            |||||||||||||||||||||||||| || ||||| || ||||||||||| || ||||||
SBJCT: 4244 ACCCTGCTGGGCTCCAATGACCTCACAGCTGTCCGACCACTGAGCTGTGACTCGAGCATG 4303

QUERY: 4378 GATGTAGCCCAGGTTCGTCTGGAGTGGCCAACAGACCTTGCTGTCAATCCCATGGATAAC 4437
            || || |||||||| ||||| || ||||| |||||||| || ||||| |||||||| |||
SBJCT: 4304 GACGTGGCCCAGGTCCGTCTAGAATGGCCGACAGACCTCGCCGTCAACCCCATGGACAAC 4363

QUERY: 4438 TCCTTGTATGTTCTAGAGAACAATGTCATCCTTCGAATCACCGAGAACCACCAAGTCAGC 4497
            ||| |||| ||||| |||||||| |||||||| || ||||| ||||||||||| ||||||
SBJCT: 4364 TCCCTGTACGTTCTGGAGAACAACGTCATCCTGCGGATCACGGAGAACCACCAGGTCAGC 4423

QUERY: 4498 ATCATTGCGGGACGCCCCATGCACTGCCAAGTTCCTGGCATTGACTACTCACTCAGCAAA 4557
            ||||| |||||||| || ||||||||||| ||||| ||||| |||||||| |||||||||
SBJCT: 4424 ATCATCGCGGGACGGCCTATGCACTGCCAGGTTCCCGGCATCGACTACTCGCTCAGCAAA 4483

QUERY: 4558 CTAGCCATTCACTCTGCCCTGGAGTCAGCCAGTGCCATTGCCATTTCTCACACTGGGGTC 4617
            || ||||| |||||||| ||||| |||||||| ||||||||||||||||||||||||||
SBJCT: 4484 CTCGCCATCCACTCTGCGCTGGAATCAGCCAGCGCCATTGCCATTTCTCACACTGGGGTG 4543

QUERY: 4618 CTCTACATCACTGAGACAGATGAGAAGAAGATTAACCGTCTACGCCAGGTAACAACCAAC 4677
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SBJCT: 4544 CTCTACATCACTGAGACGGACGAGAAGAAGATCAACCGCCTACGCCAAGTCACCACCAAT 4603

QUERY: 4678 GGGGAGATCTGCCTTTTAGCTGGGGCAGCCTCGGACTGCGACTGCAAAAACGATGTCAAT 4737
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SBJCT: 4604 GGAGAGATCTGCCTCTTAGCCGGGGCGGCCTCAGACTGTGACTGCAAAAACGATGTCAAC 4663

QUERY: 4738 TGCAACTGCTATTCAGGAGATGATGCCTACGCGACTGATGCCATCTTGAATTCCCCATCA 4797
            |||| |||||| || |||||||| || ||||| || || |||||| |||| || || ||
SBJCT: 4664 TGCATCTGCTACTCGGGAGATGACGCTTACGCCACGGACGCCATCCTGAACTCGCCGTCC 4723

QUERY: 4798 TCCTTAGCTGTAGCTCCAGATGGTACCATTTACATTGCAGACCTTGGAAATATTCGGATC 4857
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SBJCT: 4724 TCCTTAGCCGTGGCTCCGGATGGCACCATCTACATTGCAGACCTTGGGAATATCCGGATC 4783

QUERY: 4858 AGGGCGGTCAGCAAGAACAAGCCTGTTCTTAATGCCTTCAACCAGTATGAGGCTGCATCC 4917
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SBJCT: 4784 AGGGCGGTCAGCAAAAATAAACCCGTTCTTAACGCATTCAACCAGTATGAGGCTGCATCT 4843

QUERY: 4918 CCCGGAGAGCAGGAGTTATATGTTTTCAACGCTGATGGCATCCACCAATACACTGTGAGC 4977
            || ||||| ||||| || || || |||||||||||||| ||||| || |||||||||||
SBJCT: 4844 CCGGGAGAACAGGAATTGTACGTGTTCAACGCTGATGGTATCCATCAGTACACTGTGAGT 4903

QUERY: 4978 CTGGTGACAGGGGAGTACTTGTACAATTTCACATATAGTACTGACAATGATGTCACTGAA 5037
            |||||||| ||||||||||||||||||||||||||| ||  |||||||||| ||||| ||
SBJCT: 4904 CTGGTGACTGGGGAGTACTTGTACAATTTCACATACAGCGCTGACAATGACGTCACCGAG 4963

QUERY: 5038 TTGATTGACAATAATGGGAATTCCCTGAAGATCCGTCGGGACAGCAGTGGCATGCCCCGT 5097
            ||||||||||| || ||||||||||| |||||||| ||||||||||||||||||||||||
SBJCT: 4964 TTGATTGACAACAACGGGAATTCCCTAAAGATCCGCCGGGACAGCAGTGGCATGCCCCGC 5023

QUERY: 5098 CACCTGCTCATGCCTGACAACCAGATCATCACCCTCACCGTGGGCACCAATGGAGGCCTC 5157
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SBJCT: 5024 CACCTGCTCATGCCGGATAATCAGATTATCACCCTTACTGTGGGCACCAATGGAGGCCTC 5083

QUERY: 5158 AAAGTCGTGTCCACACAGAACCTGGAGCTTGGTCTCATGACCTATGATGGCAACACTGGG 5217
            |||| ||||||||| |||||||||||||||| || |||||||| |||||||| ||||||||
SBJCT: 5084 AAAGCCGTGTCCACTCAGAACCTGGAGCTGGGCCTCATGACTTATGATGGGAACACTGGA 5143

QUERY: 5218 CTCCTGGCCACCAAGAGCGATGAAACAGGATGGACGACTTTCTATGACTATGACCACGAA 5277
            ||||| ||||||||||| |||||||| |||||||| ||||| ||||||||||||||||||
SBJCT: 5144 CTCCTAGCCACCAAGAGTGATGAAACCGGATGGACAACTTTTTATGACTATGACCACGAG 5203

QUERY: 5278 GGCCGCCTGACCAACGTGACGCGCCCCACGGGGGTGGTAACCAGTCTGCACCGGGAAATG 5337
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SBJCT: 5204 GGCCGTCTGACCAATGTGACCCGCCCCACGGGCGTGGTGACCAGTCTGCACCGGGAAATG 5263

QUERY: 5338 GAGAAATCTATTACCATTGACATTGAGAACTCCAACCGTGATGATGACGTCACTGTCATC 5397
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SBJCT: 5264 GAGAAATCTATCACCATTGACATTGAGAACTCCAACCGGGATGATGACGTCACTGTGATC 5323

QUERY: 5398 ACCAACCTCTCTTCAGTAGAGGCCTCCTACACAGTGGTACAAGATCAAGTTCGGAACAGC 5457
            ||||||||||| || || ||||||||||| |||||||||||||||||||| || ||||||
SBJCT: 5324 ACCAACCTCTCCTCCGTGGAGGCCTCCTATACAGTGGTACAAGATCAAGTGCGAAACAGC 5383

QUERY: 5458 TACCAGCTCTGTAATAATGGTACCCTGAGGGTGATGTATGCTAATGGGATGGGTATCAGC 5517
            ||||||||||| |||||||| |||||| |||||||||| || || || |||| | |||||
SBJCT: 5384 TACCAGCTCTGCAATAATGGAACCCTGCGGGTGATGTACGCCAACGGCATGGCTGTCAGC 5443

QUERY: 5518 TTCCACAGCGAGCCCCATGTCCTAGCGGGCACCATCACCCCCACCATTGGACGCTGCAAC 5577
            |||||||| |||||||| ||||| || |||||||||||||||||||| || |||||||||
SBJCT: 5444 TTCCACAGTGAGCCCCACGTCCTCGCAGGCACCATCACCCCCACCATCGGGCGCTGCAAC 5503

QUERY: 5578 ATCTCCCTGCCTATGGAGAATGGCTTAAACTCCATTGAGTGGCGCCTAAGAAAGGAACAG 5637
            ||||| ||||| |||||||||||| | |||||||| ||||||||||| || |||||||||
SBJCT: 5504 ATCTCTCTGCCCATGGAGAATGGCCTGAACTCCATCGAGTGGCGCCTGAGGAAGGAACAG 5563

QUERY: 5638 ATTAAAGGCAAAGTCACCATCTTTGGCAGGAAGCTCCGGGTCCATGGAAGAAATCTCTTG 5697
            || |||||||||||||||||||||| |||||||| ||||||||| ||||| |||||| ||
SBJCT: 5564 ATCAAAGGCAAAGTCACCATCTTTGGGAGGAAGCTTCGGGTCCACGGAAGGAATCTCCTG 5623

QUERY: 5698 TCCATTGACTATGATCGAAATATTCGGACTGAAAAGATCTATGATGACCACCGGAAGTTC 5757
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SBJCT: 5624 TCCATTGATTATGACCGAAATATCCGTACGGAGAAGATCTACGATGACCACCGGAAATTC 5683

QUERY: 5758 ACCCTGAGGATCATTTATGACCAGGTGGGCCGCCCCTTCCTCTGGCTGCCCAGCAGCGGG 5817
            |||||||||||||| ||||||||||||||||||||||||||| ||||| || ||||| |||
SBJCT: 5684 ACCCTGAGGATCATCTATGACCAGGTGGGCCGCCCCTTCCTGTGGCTCCCGAGCAGTGGG 5743

QUERY: 5818 CTGGCAGCTGTCAACGTGTCATACTTCTTCAATGGGCGCCTGGCTGGGCTTCAGCGTGGG 5877
            |||||||| ||||| || || ||||||||||||||||||| |||| || || ||||| |||
SBJCT: 5744 CTGGCAGCCGTCAATGTCTCCTACTTCTTCAATGGGCGCTTGGCCGGCCTCCAGCGAGGG 5803
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QUERY: 5878 GCCATGAGCGAGAGGACAGACATCGACAAGCAAGGCCGCATCGTGTCCCGCATGTTCGCT 5937
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SBJCT: 5804 GCCATGAGCGAGAGGACAGACATTGACAAGCAAGGCCGGATCGTGTCCCGCATGTTCGCC 5863

QUERY: 5938 GACGGGAAAGTGTGGAGCTACTCCTACCTTGACAAGTCCATGGTCCTCCTGCTTCAGAGC 5997
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SBJCT: 5864 GACGGGAAAGTCTGGAGTTATTCCTATCTTGACAAGTCCATGGTCCTTCTGCTACAGAGC 5923

QUERY: 5998 CAACGTCAGTATATATTTGAGTATGACTCCTCTGACCGCCTCCTTGCCGTCACCATGCCC 6057
            ||||||||||| |||||||| ||||||||||| || |||||||  || ||||| ||||||
SBJCT: 5924 CAACGTCAGTACATATTTGAATATGACTCCTCCGATCGCCTCCACGCAGTCACTATGCCC 5983

QUERY: 6058 AGCGTGGCCCGGCACAGCATGTCCACACACACCTCCATCGGCTACATCCGTAATATTTAC 6117
            || || |||||||||||||||||||| ||||||||||| || |||||||| || ||||||
SBJCT: 5984 AGTGTCGCCCGGCACAGCATGTCCACGCACACCTCCATTGGTTACATCCGAAACATTTAC 6043

QUERY: 6118 AACCCGCCTGAAAGCAATGCTTCGGTCATCTTTGACTACAGTGATGACGGCCGCATCCTG 6177
            ||||| || ||||||||||| |||||||||||||||||||||||||||||||||||||| 
SBJCT: 6044 AACCCACCCGAAAGCAATGCATCGGTCATCTTTGACTACAGTGATGACGGCCGCATCCTA 6103

QUERY: 6178 AAGACCTCCTTTTTGGGCACCGGACGCCAGGTGTTCTACAAGTATGGGAAACTCTCCAAG 6237
            ||||| || || |||||||| || ||||||||||||||||||||||| ||||||||||||
SBJCT: 6104 AAGACATCTTTCTTGGGCACTGGGCGCCAGGTGTTCTACAAGTATGGAAAACTCTCCAAG 6163

QUERY: 6238 TTATCAGAGATTGTCTACGACAGTACCGCCGTCACCTTCGGGTATGACGAGACCACTGGT 6297
            ||||||||||| ||||||||||| || ||||||||||| ||||||||||||||||| |||
SBJCT: 6164 TTATCAGAGATAGTCTACGACAGCACAGCCGTCACCTTTGGGTATGACGAGACCACCGGT 6223

QUERY: 6298 GTCTTGAAGATGGTCAACCTCCAAAGTGGGGGCTTCTCCTGCACCATCAGGTACCGGAAG 6357
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SBJCT: 6224 GTCCTGAAGATGGTCAATCTCCAAAGTGGGGGCTTCTCCTGTACCATCAGGTACCGAAAG 6283

QUERY: 6358 ATTGGCCCCCTGGTGGACAAGCAGATCTACAGGTTCTCCGAGGAAGGCATGGTCAATGCC 6417
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SBJCT: 6284 GTTGGGCCCCTTGTGGACAAGCAGATTTACAGGTTCTCTGAGGAAGGAATGATCAACGCC 6343

QUERY: 6418 AGGTTTGACTACACCTATCATGACAACAGCTTCCGCATCGCAAGCATCAAGCCCGTCATA 6477
            |||||||| || |||||||| ||||| ||||||||||| || |||||||| |||||||| 
SBJCT: 6344 AGGTTTGATTATACCTATCACGACAATAGCTTCCGCATTGCCAGCATCAAACCCGTCATT 6403

QUERY: 6478 AGTGAGACTCCCCTCCCCGTTGACCTCTACCGCTATGATGAGATTTCTGGCAAGGTGGAA 6537
            || ||||||||||| || |||||||||||||||||||| |||||||| ||||||||||||
SBJCT: 6404 AGCGAGACTCCCCTTCCTGTTGACCTCTACCGCTATGACGAGATTTCCGGCAAGGTGGAA 6463

QUERY: 6538 CACTTTGGTAAGTTTGGAGTCATCTATTATGACATCAACCAGATCATCACCACTGCCGTG 6597
            ||||| || |||||||| |||||||| || ||||||||||||||||||||||||||||| 
SBJCT: 6464 CACTTCGGCAAGTTTGGGGTCATCTACTACGACATCAACCAGATCATCACCACTGCCGTC 6523

QUERY: 6598 ATGACCCTCAGCAAACACTTCGACACCCATGGGCGGATCAAGGAGGTCCAGTATGAGATG 6657
            ||||| || ||||| ||||| |||||||||||||| |||||||| || || |||||||||
SBJCT: 6524 ATGACGCTTAGCAAGCACTTTGACACCCATGGGCGCATCAAGGAAGTGCAATATGAGATG 6583

QUERY: 6658 TTCCGGTCCCTCATGTACTGGATGACGGTGCAATATGACAGCATGGGCAGGGTGATCAAG 6717
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SBJCT: 6584 TTCCGGTCCCTCATGTACTGGATGACTGTGCAATATGACAGTATGGGTAGGGTCATCAAG 6643

QUERY: 6718 AGGGAGCTAAAACTGGGGCCCTATGCCAATACCACGAAGTACACCTATGACTACGATGGG 6777
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SBJCT: 6644 AGGGAACTGAAACTAGGGCCCTATGCCAACACCACAAAGTACACCTATGACTATGACGGG 6703

QUERY: 6778 GACGGGCAGCTCCAGAGCGTGGCCGTCAATGACCGCCCGACCTGGCGCTACAGCTATGAC 6837
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SBJCT: 6704 GACGGCCAGCTCCAGAGTGTGGCCGTCAATGACCGGCCTACCTGGCGCTATAGCTATGAC 6763

QUERY: 6838 CTTAATGGGAATCTCCACTTACTGAACCCAGGCAACAGTGTGCGCCTCATGCCCTTGCGC 6897
            || |||||||| || ||| | || |||||||| |||||||  |||||||||||||| |||
SBJCT: 6764 CTCAATGGGAACCTGCACCTTCTAAACCCAGGAAACAGTGCTCGCCTCATGCCCTTACGC 6823

QUERY: 6898 TATGACCTCCGGGATCGGATAACCAGACTCGGGGATGTGCAGTACAAAATTGACGACGAT 6957
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SBJCT: 6824 TATGACCTCCGTGACCGGATAACCAGGCTAGGGGACGTGCAGTACAAAATCGATGACGAT 6883

QUERY: 6958 GGCTATCTGTGCCAGAGAGGGTCTGACATCTTCGAATACAATTCCAAGGGCCTCCTAACA 7017
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SBJCT: 6884 GGCTATTTGTGCCAGAGAGGGTCAGACATCTTTGAATACAACTCCAAGGGCCTTCTGACG 6943

QUERY: 7018 AGAGCCTACAACAAGGCCAGCGGGTGGAGTGTCCAGTACCGCTATGATGGCGTAGGACGG 7077
            ||||| ||||||||||||||||| ||||| || |||||||||||||| || || || ||
SBJCT: 6944 AGAGCATACAACAAGGCCAGCGGATGGAGCGTGCAGTACCGCTATGACGGAGTGGGCCGC 7003

QUERY: 7078 CGGGCTTCCTACAAGACCAACCTGGGCCACCACCTGCAGTACTTCTACTCTGACCTCCAC 7137
            ||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
SBJCT: 7004 CGGGCTTCCTACAAGACCAACCTGGGCCACCACCTACAGTACTTCTACTCCGACCTCCAC 7063

QUERY: 7138 AACCCGACGCGCATCACCCATGTCTACAATCACTCCAACTCGGAGATTACCTCACTGTAC 7197
            ||||| || || ||||||||||| ||||| ||||||||||| ||||| ||||| || |||
SBJCT: 7064 AACCCCACACGTATCACCCATGTTTACAACCACTCCAACTCTGAGATCACCTCGCTCTAC 7123

QUERY: 7198 TACGACCTCCAGGGCCACCTCTTTGCCATGGAGAGCAGCAGTGGGGAGGAGTACTATGTT 7257
            || ||||||||||||||||| ||||||||||||||||| ||||| || || ||||||||
SBJCT: 7124 TATGACCTCCAGGGCCACCTATTTGCCATGGAGAGCAGTAGTGGTGAAGAATACTATGTC 7183

QUERY: 7258 GCCTCTGATAACACAGGGACTCCTCTGGCTGTGTTCAGCATCAACGGCCTCATGATCAAA 7317
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SBJCT: 7184 GCCTCAGACAACACGGGGACCCCTCTGGCTGTGTACAGTATCAATGGCCTCATGATCAAG 7243

QUERY: 7318 CAGCTGCAGTACACGGCCTATGGGGAGATTTATTATGACTCCAACCCCGACTTCCAGATG 7377
            || ||||||||||| |||||||||||||| || ||||||||||| || ||||||||||||
SBJCT: 7244 CAACTGCAGTACACAGCCTATGGGGAGATCTACTATGACTCCAATCCAGACTTCCAGATG 7303

QUERY: 7378 GTCATTGGCTTCCATGGGGGACTCTATGACCCCCTGACCAAGCTGGTCCACTTCACTCAG 7437
            |||||||||||||| || || |||||||||||||| |||||||| |||||||| |||||
SBJCT: 7304 GTCATTGGCTTCCACGGAGGCCTCTATGACCCCCTCACCAAGCTCGTCCACTTTACTCAA 7363

QUERY: 7438 CGTGATTATGATGTGCTGGCAGGACGATGGACCTCCCCAGACTATACCATGTGGAAAAAC 7497
            ||||||||||| |||||||||||||| ||||| ||||| ||||| ||||||||||  |||
SBJCT: 7364 CGTGATTATGACGTGCTGGCAGGACGGTGGACGTCCCCCGACTACACCATGTGGAGGAAC 7423

QUERY: 7498 GTGGGCAAGGAGCCGGCCCCCTTTAACCTGTATATGTTCAAGAGCAACAATCCTCTCAGC 7557
            |||||||||||||| |||||||| |||||||| |||||||||| |||||||||||| |||
SBJCT: 7424 GTGGGCAAGGAGCCAGCCCCCTTCAACCTGTACATGTTCAAGAACAACAATCCTCTGAGC 7483

QUERY: 7558 AGTGAGCTAGATTTGAAGAACTACGTGACAGATGTGAAAAGCTGGCTTGTGATGTTTGGA 7617
            | |||||| || || ||||||||||||||||| ||||| |||||||||||||||||||||
SBJCT: 7484 AATGAGCTGGACTTAAAGAACTACGTGACAGACGTGAAGAGCTGGCTTGTGATGTTTGGA 7543

QUERY: 7618 TTTCAGCTTAGCAACATCATTCCTGGCTTCCCGAGAGCCAAAATGTATTTCGTGCCTCCT 7677
            |||||||| ||||||||||||||||| ||||||||||||||||||||||| ||||||||
SBJCT: 7544 TTTCAGCTCAGCAACATCATTCCTGGATTCCCGAGAGCCAAAATGTATTTTGTGCCTCCC 7603

QUERY: 7678 CCCTATGAATTGTCAGAGAGTCAAGCAAGTGAGAATGGACAGCTCATTACAGGTGTCCAA 7737
            ||||||||| ||||||||||||||||||| ||||| |||||||||||||||||||||||
SBJCT: 7604 CCCTATGAACTGTCAGAGAGTCAAGCAAGCGAGAACGGACAGCTCATTACAGGTGTCCAG 7663

QUERY: 7738 CAGACAACAGAGAGACATAACCAGGCCTTCATGGCTCTGGAAGGACAGGTCATTACTAAA 7797
            |||||||| ||||| ||||||||||||||| |||||||||||||||||||||| ||||||
SBJCT: 7664 CAGACAACTGAGAGGCATAACCAGGCCTTCCTGGCTCTGGAAGGACAGGTCATCACTAAA 7723

QUERY: 7798 AAGCTCCACGCCAGCATCCGAGAGAAAGCAGGTCACTGGTTTGCCACCACCACGCCCATC 7857
            |||||||| ||||||||||||||||||||||| ||||||||||| |||||||| ||||||
SBJCT: 7724 AAGCTCCATGCCAGCATCCGAGAGAAAGCAGGCCACTGGTTTGCTACCACCACACCCATC 7783

QUERY: 7858 ATTGGCAAAGGCATCATGTTTGCCATCAAAGAAGGGCGGGTGACCACGGGCGTGTCCAGC 7917
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SBJCT: 7784 ATCGGCAAAGGCATCATGTTTGCCATCAAAGAAGGGCGGGTGACCACAGGAGTGTCTAGC 7843

QUERY: 7918 ATCGCCAGCGAAGATAGCCGCAAGGTGGCATCTGTGCTGAACAACGCCTACTACCTGGAC 7977
            |||||||| || || ||||||||||| ||||| ||| ||||||| ||||||||| | |||
SBJCT: 7844 ATCGCCAGTGAGGACAGCCGCAAGGTAGCATCCGTGTTGAACAATGCCTACTACTTAGAC 7903
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QUERY: 7978 AAGATGCACTACAGCATCGAGGGCAAGGACACCCACTACTTTGTGAAGATTGGCTCAGCC 8037
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SBJCT: 7904 AAGATGCACTACAGCATCGAGGGCAAGGACACACACTACTTTGTGAAGATCGGCGCCGCG 7963

QUERY: 8038 GATGGCGACCTGGTCACACTAGGCACCACCATCGGCCGCAAGGTGCTAGAGAGCGGGGTG 8097
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QUERY: 8098 AACGTGACCGTGTCCCAGCCCACGCTGCTGGTCAACGGCAGGACTCGAAGGTTCACGAAC 8157
            |||||||| ||||| |||||||||||||||||| || |||||||||||||||||| |||
SBJCT: 8024 AACGTGACGGTGTCACAGCCCACGCTGCTGGTGAATGGCAGGACTCGAAGGTTCACCAAC 8083

QUERY: 8158 ATTGAGTTCCAGTACTCCACGCTGCTGCTCAGCATCCGCTATGGCCTCACCCCCGACACC 8217
            |||||||||||||||||||||||||||||||| |||||||| ||||||||||||||||| 
SBJCT: 8084 ATTGAGTTCCAGTACTCCACGCTGCTGCTCAGTATCCGCTACGGCCTCACCCCCGACACG 8143

QUERY: 8218 CTGGACGAAGAGAAGGCCCGCGTCCTGGACCAGGCGAGACAGAGGGCCCTGGGCACGGCC 8277
            ||||||||||| |||||||||||||||||||| ||| ||||||| ||||||||| || |||
SBJCT: 8144 CTGGACGAAGAAAAGGCCCGCGTCCTGGACCAAGCGGGACAGAGAGCCCTGGGTACTGCC 8203

QUERY: 8278 TGGGCCAAGGAGCAGCAGAAAGCCAGGGACGGGAGAGAGGGGAGCCGCCTGTGGACTGAG 8337
            ||||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
SBJCT: 8204 TGGGCCAAGGAGCAGCAGAAAGCCAGGGACGGGAGAGAGGGCAGCCGCCTGTGGACGGAG 8263

QUERY: 8338 GGCGAGAAGCAGCAGCTTCTGAGCACCGGGCGCGTGCAAGGGTACGAGGGATATTACGTG 8397
            |||||||||||||| || |||||||| || || || |||| | || ||||| |||||||| 
SBJCT: 8264 GGCGAGAAGCAGCAACTCCTGAGCACGGGACGGGTACAAGGTTATGAGGGCTATTACGTA 8323

QUERY: 8398 CTTCCCGTGGAGCAATACCCAGAGCTTGCAGACAGTAGCAGCAACATCCAGTTTTTAAGA 8457
            ||||| ||||| || ||||| ||||| ||||||||||||||||||||||||||| ||||||
SBJCT: 8324 CTTCCGGTGGAACAGTACCCGGAGCTGGCAGACAGTAGCAGCAACATCCAGTTCTTAAGA 8383

QUERY: 8458 CAGAATGAGATGGGAAAGAGGTAACAAAATAATCTGCTGCCATTCCTTGTCTGAATGGCT 8517
            |||||||||||||||||||||||||||||||| |||||||||   ||| ||||  |||||
SBJCT: 8384 CAGAATGAGATGGGAAAGAGGTAACAAAATAACCTGCTGCCACCTCTTCTCTGGGTGGCT 8443

QUERY: 8518 CAGCAGGAGTAACTGTTATCTCCTCTCCTAAGGAGATGAAGACCTAACAGGGGCACTGCG 8577
            ||||||||| |||||| | |||||||||||||||||| |||||||||||| |||||||| |
SBJCT: 8444 CAGCAGGAGCAACTGTGACCTCCTCTCCTAAGGAGACGAAGACCTAAC-GGGGCACTGAG 8502

QUERY: 8578 GCTGGGCTGCTTTAGGAGACCAAGTGGCAAGAAAGCTCACATTTTTGAGTTCAAATGCT 8637
            || ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
SBJCT: 8503 GCCGGGCTGCTTTAGGATCCCAAGTGGCAAGAAAGCTCACATTTTTGAGTTCAAATGCT 8562

QUERY: 8638 ACTGTCCAAGCGAGAAGTCCCTCATCCTGAAGTAGACTAAAGCCCGGC 8685
            |||||| |||||| | ||||||||||||||||||||||||| ||||||||
SBJCT: 8563 ACTGTCTAAGCGCAAAGTCCCTCATCCTGAAGTAGACTAGAGCCCGGC 8610
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SCORE = 1570 BITS (792), EXPECT = 0.0
IDENTITIES = 1095/1196 (91%)
STRAND = PLUS / PLUS

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QUERY: 270  ATCTGGAATAATGGATGTAAAGGACCGGCGACACCGCTCTTTGACCAGAGGACGCTGTGG 329
            ||||||||||||||||||||||||||||||||| |||||||||||||| ||||| |||||
SBJCT: 103  ATCTGGAATAATGGATGTAAAGGACCGGCGACATCGCTCTTTGACCAGGGGACGGTGTGG 162

QUERY: 330  CAAAGAGTGTCGCTACACAAGCTCCTCTCTGGACAGTGAGGACTGCCGGGTGCCCACACA 389
            |||||||||||||||||| |||||||||||||||||||||||||||||| |||||||| ||
SBJCT: 163  CAAAGAGTGTCGCTACACCAGCTCCTCTCTGGACAGTGAGGACTGCCGTGTGCCCACTCA 222

QUERY: 390  GAAATCCTACAGCTCCAGTGAGACTCTGAAGGCCTATGACCATGACAGCAGGATGCACTA 449
            ||| |||||||| |||||||||||  ||||||| |||||||||||||||||| ||||||||
SBJCT: 223  GAAGTCCTACAGTTCCAGTGAGACCTTGAAGGCTTATGACCATGACAGCAGAATGCACTA 282

QUERY: 450  TGGAAACCGAGTCACAGACCTCATCCACCGGGAGTCAGATGAGTTTCCTAGACAAGGAAC 509
            |||||||||||||||||||||  | ||||||||||| ||||||||| ||||||||||| ||
SBJCT: 283  TGGAAACCGAGTCACAGACCTGGTGCACCGGGAGTCCGATGAGTTTTCTAGACAAGGGAC 342

QUERY: 510  CAACTTCACCCTTGCCGAACTGGGCATCTGTGAGCCCTCCCCACACCGAAGCGGCTACTG 569
             ||||||||||| || ||| |||| ||||| |||||||||||||||||||| || |||||
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SBJCT: 343  AAACTTCACCCTGGCAGAATTGGGAATCTGCGAGCCCTCCCCACACCGAAGTGGTTACTG 402

QUERY: 570  CTCCGACATGGGGATCCTTCACCAGGGCTACTCCCTTAGCACAGGGTCTGACGCCGACTC 629
             ||||||||||| ||||| ||||||||||||||||| ||||| |||||||| || |||||
SBJCT: 403  TTCCGACATGGGTATCCTCCACCAGGGCTACTCCCTGAGCACTGGGTCTGATGCAGACTC 462

QUERY: 630  CGACACCGAGGGAGGGATGTCTCCAGAACACGCCATCAGACTGTGGGGCAGAGGGATAAA 689
             ||||||||||||||||||||||||||||| |||||||||||||||||  ||||||||||
SBJCT: 463  GGACACCGAGGGAGGGATGTCTCCAGAACATGCCATCAGACTGTGGGGACGAGGGATAAA 522

QUERY: 690  ATCCAGGCGCAGTTCCGGCCTGTCCAGTCGTGAAAACTCGGCCCTTACCCTGACTGACTC 749
            |||||||||||| || ||| ||||||| || || |||||||||||||| |||||||||||
SBJCT: 523  ATCCAGGCGCAGCTCTGGCTTGTCCAGCCGCGAGAACTCGGCCCTTACTCTGACTGACTC 582

QUERY: 750  TGACAACGAAAACAAATCAGATGATGAGAACGGTCGTCCCATTCCACCTACATCCTCGCC 809
            |||||| ||||| ||||| ||||| || || ||||||||||||||||||||||||||| |
SBJCT: 583  TGACAATGAAAATAAATCGGATGACGACAATGGTCGTCCCATTCCACCTACATCCTCGTC 642

QUERY: 810  TAGTCTCCTCCCATCTGCTCAGCTGCCTAGCTCCCATAATCCTCCACCAGTTAGCTGCCA 869
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 643  TAGCCTCCTCCCATCTGCTCAGCTGCCTAGCTCCCATAATCCTCCACCAGTTAGCTGCCA 702

QUERY: 870  GATGCCATTGCTAGACAGCAACACCTCCCATCAAATCATGGACACCAACCCTGATGAGGA 929
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
SBJCT: 703  GATGCCATTGCTAGACAGCAACACCTCCCATCAGATCATGGACACCAACCCTGATGAGGA 762

QUERY: 930  ATTCTCCCCCAATTCATACCTGCTCAGAGCATGCTCAGGGCCCCAGCAAGCCTCCAGCAG 989
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 763  ATTCTCCCCCAATTCATACCTGCTCAGAGCATGCTCAGGGCCCCAGCAAGCCTCCAGCAG 822

QUERY: 990  TGGCCCTCCGAACCACCACAGCCAGTCGACTCTGAGGCCCCCTCTCCCACCCCCTCACAA 1049
            ||||||||| ||||||||||||||||| || |||||||||||||| ||||||||||| ||
SBJCT: 823  TGGCCCTCCAAACCACCACAGCCAGTCAACACTGAGGCCCCCTCTGCCACCCCCTCATAA 882

QUERY: 1050 CCACACGCTGTCCCATCACCACTCGTCCGCCAACTCCCTCAACAGGAACTCACTGACCAA 1109
            |||||| |||||||| |||||||| || ||||||||||||||||||||||||||||||||
SBJCT: 883  CCACACCCTGTCCCACCACCACTCCTCGGCCAACTCCCTCAACAGGAACTCACTGACCAA 942

QUERY: 1110 TCGGCGGAGTCAGATCCACGCCCCGGCCCCAGCGCCCAATGACCTGGCCACCACACCAGA 1169
            |||||||||||| ||||||||||| || || |||||||| |||||||||||||| |||||
SBJCT: 943  TCGGCGGAGTCAAATCCACGCCCCAGCTCCTGCGCCCAACGACCTGGCCACCACCCCAGA 1002

QUERY: 1170 GTCCGTTCAGCTTCAGGACAGCTGGGTGCTAAACAGCAACGTGCCACTGGAGACCCGGCA 1229
            ||| |||||||| ||||| ||||||||||| ||||| ||||| ||||||||||| |||||
SBJCT: 1003 GTCTGTTCAGCTCCAGGATAGCTGGGTGCTGAACAGTAACGTCCCACTGGAGACTCGGCA 1062

QUERY: 1230 CTTCCTCTTCAAGACCTCCTCGGGGAGCACACCCTTGTTCAGCAGCTCTTCCCCGGGATA 1289
            |||||| ||||| || || || || ||||||||| |||||||||||||||| ||||||||
SBJCT: 1063 CTTCCTTTTCAAAACGTCGTCTGGAAGCACACCCCTGTTCAGCAGCTCTTCTCCGGGATA 1122

QUERY: 1290 CCCTTTGACCTCAGGAACGGTTTACACGCCCCCGCCCCGCCTGCTGCCCAGGAATACTTT 1349
            ||||||||||||||| || ||||| || || || ||||||||||||||  ||||||| ||
SBJCT: 1123 CCCTTTGACCTCAGGGACCGTTTATACACCACCACCCCGCCTGCTGCCACGGAATACATT 1182

QUERY: 1350 CTCCAGGAAGGCTTTCAAGCTGAAGAAGCCCTCCAAATACTGCAGCTGGAAATGTGCTGC 1409
            |||||||||||| |||||||||||||| ||||||||||||||||| ||||||||||||||
SBJCT: 1183 CTCCAGGAAGGCCTTCAAGCTGAAGAAACCCTCCAAATACTGCAGTTGGAAATGTGCTGC 1242

QUERY: 1410 CCTCTCCGCCATTGCCGCGGCCCTCCTCTTGGCTATTTTGCTGGCGTATTTCATAG 1465
            ||| || ||||| ||||| |||||||||||||| ||||||||||| ||||||||||
SBJCT: 1243 CCTGTCTGCCATCGCCGCCGCCCTCCTCTTGGCCATTTTGCTGGCATATTTCATAG 1298
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 SCORE = 1455 BITS (734), EXPECT = 0.0
 IDENTITIES = 1000/1088 (91%), GAPS = 3/1088 (0%)
 STRAND = PLUS / PLUS
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QUERY: 1464 AGTGCCCTGGTCGTTGAAAAACAGCAGCATAGACAGTGGTGAAGCAGAAGTTGGTCGGCG 1523
            |||||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||
SBJCT: 1420 AGTGCCCTGGTCATTGAAAAACAGCAGCATAGACAGTGGCGAAGCAGAAGTTGGTCGGCG 1479
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QUERY: 1524 GGTAACACAAGAAGTCCCACCAGGGGTGTTTTGGAGGTCACAAATTCACATCAGTCAGCC 1583
            ||| ||||| ||||||||||||||||||||||||||||| || |||||||||||||||||
SBJCT: 1480 GGTGACACAGGAAGTCCCACCAGGGGTGTTTTGGAGGTCCCAGATTCACATCAGTCAGCC 1539

QUERY: 1584 CCAGTTCTTAAAGTTCAACATCTCCCTCGGGAAGGACGCTCTCTTTGGTGTTTACATAAG 1643
             || ||||||||||||||||||||||| || ||||| || ||||| ||||| || |||||
SBJCT: 1540 TCAATTCTTAAAGTTCAACATCTCCCTGGGCAAGGATGCCCTCTTCGGTGTCTATATAAG 1599

QUERY: 1644 AAGAGGACTTCCACCATCTCATGCCCAGTATGACTTCATGGAACGTCTGGACGGGAAGGA 1703
             |||||||| ||||| ||||||||||||||||||||||||||||| ||||| || |||||
SBJCT: 1600 GAGAGGACTACCACCGTCTCATGCCCAGTATGACTTCATGGAACGCCTGGATGGAAAGGA 1659

QUERY: 1704 GAAGTGGAGTGTGGTTGAGTCTCCCAGGGAACGCCGGAGCATACAGACCTTGGTTCAGAA 1763
            ||| ||||| ||||| ||||| |||||||||||||||||||| |||||  |||| |||||
SBJCT: 1660 GAAATGGAGCGTGGTCGAGTCGCCCAGGGAACGCCGGAGCATCCAGACTCTGGTGCAGAA 1719

QUERY: 1764 TGAAGCCGTGTTTGTGCAGTACCTGGATGTGGGCCTGTGGCATCTGGCCTTCTACAATGA 1823
             || || ||||||||||||||| ||||||||||||||||||| |||||||||||||||||
SBJCT: 1720 CGAGGCTGTGTTTGTGCAGTACTTGGATGTGGGCCTGTGGCACCTGGCCTTCTACAATGA 1779

QUERY: 1824 TGGAAAAGACAAAGAGATGGTTTCCTTCAATACTGTTGTCCTAGATTCAGTGCAGGACTG 1883
             || || ||||| |||||||| |||||||| ||||||||| |||||||||||||||||||
SBJCT: 1780 CGGCAAGGACAAGGAGATGGTCTCCTTCAACACTGTTGTCTTAGATTCAGTGCAGGACTG 1839

QUERY: 1884 TCCACGTAACTGCCATGGGAATGGTGAATGTGTGTCCGGGGTGTGTCACTGTTTCCCAGG 1943
            |||||| ||||| || ||||| |||||||| ||||| ||  |||||||||||||||||||
SBJCT: 1840 TCCACGGAACTGTCACGGGAACGGTGAATGCGTGTCTGGACTGTGTCACTGTTTCCCAGG 1899

QUERY: 1944 ATTTCTAGGAGCAGACTGTGCTAAAGCTGCCTGCCCTGTCCTGTGCAGTGGGAATGGACA 2003
            ||| ||||| ||||||||||||||||||||||||||||| |||||||| || ||||||||
SBJCT: 1900 ATTCCTAGGTGCAGACTGTGCTAAAGCTGCCTGCCCTGTACTGTGCAGCGGAAATGGACA 1959

QUERY: 2004 ATATTCTAAAGGGACGTGCCAGTGCTACAGCGGCTGGAAAGGTGCAGAGTGCGACGTGCC 2063
             ||||||||||| |||||||||||||||||||||||||||||||||||||| || |||||
SBJCT: 1960 GTATTCTAAAGGAACGTGCCAGTGCTACAGCGGCTGGAAAGGTGCAGAGTGTGATGTGCC 2019

QUERY: 2064 CATGAATCAGTGCATCGATCCTTCCTGCGGGGGCCACGGCTCCTGCATTGATGGGAACTG 2123
             ||||| || || ||||||||||||||| |||||||| ||||||||||||||||||||||
SBJCT: 2020 TATGAACCAATGTATCGATCCTTCCTGTGGGGGCCATGGCTCCTGCATTGATGGGAACTG 2079

QUERY: 2124 TGTCTGCTCTGCTGGCTACAAAGGCGAGCACTGTGAGGAAGTTGATTGCTTGGATCCCAC 2183
             || ||  ||||||||||||| ||||||||||||||||||||||||||||||||||| ||
SBJCT: 2080 CGTGTGTGCTGCTGGCTACAAGGGCGAGCACTGTGAGGAAGTTGATTGCTTGGATCCTAC 2139

QUERY: 2184 CTGCTCCAGCCACGGAGTCTGTGTGAATGGAGAATGCCTGTGCAGCCCTGGCTGGGGTGG 2243
            |||||||||||| || |||||||||||||||||| || | |||||||| |||||||||||
SBJCT: 2140 CTGCTCCAGCCATGGTGTCTGTGTGAATGGAGAGTGTCTATGCAGCCCCGGCTGGGGTGG 2199

QUERY: 2244 TCTGAACTGTGAGCTGGCGAGGGTCCAGTGCCCAGACCAGTGCAGTGGGCATGGCACGTA 2303
            ||| |||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
SBJCT: 2200 TCTCAACTGTGAGCTGGCGAGGGTCCAGTGCCCAGACCAGTGTAGTGGGCATGGCACTTA 2259

QUERY: 2304 CCTGCCTGACACGGGCCTCTGCAGCTGCGATCCCAACTGGATGGGTCCCGACTGCTCTGT 2363
            ||| |||||| | |||||||||||||| ||||| ||||||||||||||||||||||||||
SBJCT: 2260 CCTCCCTGACTCCGGCCTCTGCAGCTGTGATCCGAACTGGATGGGTCCCGACTGCTCTGT 2319

QUERY: 2364 TGAAGTGTGCTCAGTAGACTGTGGCACTCACGGCGTCTGCATCGGGGGAGCCTGCCGCTG 2423
            |   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2320 T---GTGTGCTCAGTAGACTGTGGCACTCACGGCGTCTGCATCGGGGGAGCCTGCCGCTG 2376

QUERY: 2424 TGAAGAGGGCTGGACAGGCGCAGCGTGTGACCAGCGCGTGTGCCACCCCCGCTGCATTGA 2483
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
SBJCT: 2377 TGAAGAGGGCTGGACAGGCGCAGCTTGTGACCAGCGCGTGTGCCACCCCCGCTGCATTGA 2436

QUERY: 2484 GCACGGGACCTGTAAAGATGGCAAATGTGAATGCCGAGAGGGCTGGAATGGTGAACACTG 2543
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2437 GCACGGGACCTGTAAAGATGGCAAATGTGAATGCCGAGAGGGCTGGAATGGTGAACACTG 2496

QUERY: 2544 CACCATTG 2551
            ||||||||
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SBJCT: 2497 CACCATTG 2504
 SCORE =  105 BITS (53), EXPECT = 5E-19
 IDENTITIES = 81/89 (91%), GAPS = 1/89 (1%)
 STRAND = PLUS / PLUS

QUERY: 8711 AACGAATGAATGAACAGACACACACAATGTTCCAAGTTCCCCTAAAATATGACCCACTTG 8770
            |||||| ||||||| | ||||||| |||||| ||||||||||||||||||||||||||||
SBJCT: 8655 AACGAACGAATGAAAACACACACAAAATGTTTCAAGTTCCCCTAAAATATGACCCACTTG 8714

QUERY: 8771 TTCTGGGTCT-ACGCAGAAAAGAGACGCA 8798
            ||| |||||| | ||||||||||||||||
SBJCT: 8715 TTCCGGGTCTAAGGCAGAAAAGAGACGCA 8743

SCORE = 48.1 BITS (24), EXPECT = 0.093
 IDENTITIES = 30/32 (93%)
 STRAND = PLUS / PLUS

QUERY: 475 CACCGGGAGTCAGATGAGTTTCCTAGACAAGG 506
           ||||||||||| ||||||||| ||||||||||
SBJCT: 7   CACCGGGAGTCCGATGAGTTTTCTAGACAAGG 38
```

In this search it was also found that the FCTR3bcd and e nucleic acids had homology to three fragments of *Rattus norvegicus* neurestin alpha. It has 5498 of 6132 bases (89%) identical to bases 2527-8658, 1081 of 1196 bases (90%) identical to bases 123-1318, 996 of 1088 bases (91%) identical to bases 1440-2527 of *Rattus norvegicus* neurestin alpha (GenBank Acc:NM_020088.1) (Table 3N).

Table 3N. BLASTN of FCTR3b, c, d, and e against *Rattus norvegicus* Neurestin alpha mRNA (SEQ ID NO:66)

```
>GI|9910319|REF|NM_020088.1| RATTUS NORVEGICUS NEURESTIN ALPHA (LOC56762), MRNA
          LENGTH = 8689

 SCORE = 7129 BITS (3596), EXPECT = 0.0
 IDENTITIES = 5498/6132 (89%)
 STRAND = PLUS / PLUS

QUERY: 2578 GATGGCTGCCCTGACTTGTGCAACGGTAACGGGAGATGCACACTGGGTCAGAACAGCTGG 2637
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2527 GATGGCTGCCCTGATTTGTGCAACGGTAACGGGAGATGCACACTGGGTCAGAACAGCTGG 2586

QUERY: 2638 CAGTGTGTCTGCCAGACCGGCTGGAGAGGGCCCGGATGCAACGTTGCCATGGAAACTTCC 2697
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
SBJCT: 2587 CAGTGTGTCTGCCAGACCGGCTGGAGAGGGCCCGGATGCAACGTTGCCATGGAAACCTCC 2646

QUERY: 2698 TGTGCTGATAACAAGGATAATGAGGGAGATGGCCTGGTGGATTGTTTGGACCCTGACTGC 2757
            || |||||||||||||||||||||||||||||||||||||| ||  ||||||||||||||
SBJCT: 2647 TGCGCTGATAACAAGGATAATGAGGGAGATGGCCTGGTGGACTGCCTGGACCCTGACTGC 2706

QUERY: 2758 TGCCTGCAGTCAGCCTGTCAGAACAGCCTGCTCTGCCGGGGGTCCCGGGACCCACTGGAC 2817
            ||||| ||||||||||||||||||||||||||||| |||||||| ||||||||  |||||
SBJCT: 2707 TGCCTCCAGTCAGCCTGTCAGAACAGCCTGCTCTGTCGGGGGTCTCGGGACCCCTTGGAC 2766

QUERY: 2818 ATCATTCAGCAGGGCCAGACGGATTGGCCCGCAGTGAAGTCCTTCTATGACCGTATCAAG 2877
            ||||||||||| |||||||| || ||||| || ||||||||||||||||| |||||||||
SBJCT: 2767 ATCATTCAGCAAGGCCAGACAGACTGGCCTGCGGTGAAGTCCTTCTATGATCGTATCAAG 2826

QUERY: 2878 CTCTTGGCAGGCAAGGATAGCACCCACATCATTCCTGGAGAGAACCCTTTCAACAGCAGC 2937
            ||||||||||||||||| ||||||||||||||||||||||| ||||| ||||| ||||||
SBJCT: 2827 CTCTTGGCAGGCAAGGACAGCACCCACATCATTCCTGGAGACAACCCCTTCAATAGCAGC 2886

QUERY: 2938 TTGGTTTCTCTCATCCGAGGCCAAGTAGTAACTACAGATGGAACTCCCCTGGTCGGTGTG 2997
             |||| ||||| |||||||||||||||||||| || ||||| | ||||||||| ||||||
SBJCT: 2887 CTGGTGTCTCTGATCCGAGGCCAAGTAGTAACCACGGATGGGACCCCCCTGGTGGGTGTG 2946
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QUERY: 2998 AACGTGTCTTTTGTCAAGTACCCAAAATACGGCTACACCATCACCCGCCAGGATGGCACG 3057
            || |||||||||||||||||||||||||| |||||||||||||| |||||||| ||||||
SBJCT: 2947 AATGTGTCTTTTGTCAAGTACCCAAAATATGGCTACACCATCACTCGCCAGGACGGCACG 3006

QUERY: 3058 TTCGACCTGATCGCAAATGGAGGTGCTTCCTTGACTCTACACTTTGAGCGAGCCCCGTTC 3117
            || |||||||| || ||||| ||  || |||||||||| ||||||||||||||||| |||
SBJCT: 3007 TTTGACCTGATTGCCAATGGGGGCTCTGCCTTGACTCTTCACTTTGAGCGAGCCCCTTTC 3066

QUERY: 3118 ATGAGCCAGGAGCGCACTGTGTGGCTGCCGTGGAACAGCTTTTACGCCATGGACACCCTG 3177
            ||||||| ||||||||| || |||| ||||||||||||||| || |||||||||||||||
SBJCT: 3067 ATGAGCCGGGAGCGCACAGTATGGCCGCCGTGGAACAGCTTCTATGCCATGGACACCCTG 3126

QUERY: 3178 GTGATGAAGACCGAGGAGAACTCCATCCCCAGCTGTGACCTCAGTGGCTTTGTCCGGCCT 3237
            || |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 3127 GTAATGAAGACGGAGGAGAACTCCATCCCCAGCTGTGACCTCAGTGGCTTTGTCCGGCCT 3186

QUERY: 3238 GATCCAATCATCATCTCCTCCCCACTGTCCACCTTCTTTAGTGCTGCCCCTGGCAGAAT 3297
            ||||| |||||||||||||| || |||||||||||||| || ||| |||||| |  ||| 
SBJCT: 3187 GATCCGATCATCATCTCCTCTCCTCTGTCCACCTTCTTCAGCGCTTCCCCTGCGGCGAAC 3246

QUERY: 3298 CCCATCGTGCCTGAGACCCAGGTTCTTCATGAAGAAATCGAGCTCCCTGGTTCCAATGTG 3357
            ||||| |||||||||||||||||||||||||| || ||||||||||||||  |||| |||
SBJCT: 3247 CCCATTGTGCCTGAGACCCAGGTTCTTCATGAGGAGATCGAGCTCCCTGGCACCAACGTG 3306

QUERY: 3358 AAACTTCGCTATCTGAGCTCTAGAACTGCAGGGTACAAGTCACTGCTGAAGATCACCATG 3417
            || || || || || ||||| ||||| |||||||||||||||||||||||||||||||||
SBJCT: 3307 AAGCTCCGTTACCTCAGCTCCAGAACAGCAGGGTACAAGTCACTGCTGAAGATCACCATG 3366

QUERY: 3418 ACCCAGTCCACAGTGCCCCTGAACCTCATTAGGGTTCACCTGATGGTGGCTGTCGAGGGG 3477
            ||||||||||| |||||| ||||||||||  |||||||| ||||||| || || ||||||
SBJCT: 3367 ACCCAGTCCACGGTGCCCTTGAACCTCATCCGGGTTCACTTGATGGTTGCCGTGGAGGGG 3426

QUERY: 3478 CATCTCTTCCAGAAGTCATTCCAGGCTTCTCCCAACCTGGCCTCCACCTTCATCTGGGAC 3537
            ||||||||||||||||| ||||||||||||||||||||||||| ||| ||||||||||||
SBJCT: 3427 CATCTCTTCCAGAAGTCGTTCCAGGCTTCTCCCAACCTGGCCTACACATTCATCTGGGAC 3486

QUERY: 3538 AAGACAGATGCGTATGGCCAAAGGGTGTATGGACTCTCAGATGCTGTTGTGTCTGTCGGG 3597
            |||||||| || |||||||||||||| ||||| || || ||||||||||||||||| || 
SBJCT: 3487 AAGACAGACGCTTATGGCCAAAGGGTTTATGGCCTATCGGATGCTGTTGTGTCTGTTGGA 3546

QUERY: 3598 TTTGAATATGAGACCTGTCCCAGTCTAATTCTCTGGGAGAAAAGGACAGCCCTCCTTCAG 3657
            ||||||||||||||||| |||||||| || || ||||| |||||||||||||| ||||| 
SBJCT: 3547 TTTGAATATGAGACCTGCCCCAGTCTCATCCTGTGGGAAAAAAGGACAGCCCTACTTCAA 3606

QUERY: 3658 GGATTCGAGCTGGACCCCTCCAACCTCGGTGGCTGGTCCCTAGACAAACACCACATCCTC 3717
            ||||||||||||||||| |||||||| |||||||||||||| || || ||||||| ||||
SBJCT: 3607 GGATTCGAGCTGGACCCTTCCAACCTTGGTGGCTGGTCCCTGGATAAGCACCACACCCTC 3666

QUERY: 3718 AATGTTAAAAGTGGAATCCTACACAAAGGCACTGGGGAAAACCAGTTCCTGACCCAGCAG 3777
            ||||| ||||| ||||| |||| ||||||||| ||||| |||||||||||||||||||||
SBJCT: 3667 AATGTGAAAAGCGGAATACTACTCAAAGGCACAGGGGAGAACCAGTTCCTGACCCAGCAG 3726

QUERY: 3778 CCTGCCATCATCACCAGCATCATGGGCAATGGTCGCCGCCGGAGCATTTCCTGTCCCAGC 3837
            || ||||||||||||||||||||||| || ||||||||| | ||||| ||||||||||||
SBJCT: 3727 CCCGCCATCATCACCAGCATCATGGGTAACGGTCGCCGCAGAAGCATCTCCTGTCCCAGC 3786

QUERY: 3838 TGCAACGGCCTTGCTGAAGGCAACAAGCTGCTGGCCCCAGTGGCTCTGGCTGTTGGAATC 3897
            ||||| |||||||||||||||||||| ||| ||||||| ||||| |||||||| || |||
SBJCT: 3787 TGCAATGGCCTTGCTGAAGGCAACAAACTGTTGGCCCCCGTGGCCCTGGCTGTGGGGATC 3846

QUERY: 3898 GATGGGAGCCTCTATGTGGGTGACTTCAATTACATCCGACGCATCTTTCCCTCTCGAAAT 3957
            ||||||||||||| ||| |||||||||||||| ||||| |||||||| || |||||||| 
SBJCT: 3847 GATGGGAGCCTCTTTGTCGGTGACTTCAATTATATCCGGCGCATCTTCCCTTCTCGAAAC 3906

QUERY: 3958 GTGACCAGCATCTTGGAGTTACGAAATAAAGAGTTTAAACATAGCAACAACCCAGCACAC 4017
            |||||||| |||||||||||||||||||||||||||||||||||||||| ||||| ||||
SBJCT: 3907 GTGACCAGTATCTTGGAGTTACGAAATAAAGAGTTTAAACATAGCAACAGCCCAGGACAC 3966

QUERY: 4018 AAGTACTACTTGGCAGTGGACCCCGTGTCCGGCTCGCTCTACGTGTCCGACACCAACAGC 4077
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             |||||||||||||| |||||||| ||| | ||||||||||| || || |||||||||||
SBJCT: 3967 AAGTACTACTTGGCTGTGGACCCTGTGACTGGCTCGCTCTATGTCTCTGACACCAACAGT 4026

QUERY: 4078 AGGAGAATCTACCGCGTCAAGTCTCTGAGTGGAACCAAAGACCTGGCTGGGAATTCGGAA 4137
              |  | |||||||| ||||||||||| || ||| ||||||||||||||||||||||||||
SBJCT: 4027 CGCCGGATCTACCGAGTCAAGTCTCTAAGCGGAGCCAAAGACCTGGCTGGGAATTCGGAA 4086

QUERY: 4138 GTTGTGGCAGGGACGGGAGAGCAGTGTCTACCCTTTGATGAAGCCCGCTGCGGGGATGGA 4197
            |||||||| ||||| || || || |||||||||||||||||||||||||| ||||||||
SBJCT: 4087 GTTGTGGCCGGGACTGGCGAACAATGTCTACCCTTTGATGAAGCCCGCTGTGGGGATGGC 4146

QUERY: 4198 GGGAAGGCCATAGATGCAACCCTGATGAGCCCGAGAGGTATTGCAGTAGACAAGAATGGG 4257
            ||||||||    | ||||| |||||||||||||| |||||||||||||||||||||| |||
SBJCT: 4147 GGGAAGGCTGTGGATGCCACCCTGATGAGCCCTAGAGGTATTGCAGTAGACAAGAACGGG 4206

QUERY: 4258 CTCATGTACTTTGTCGATGCCACCATGATCCGGAAGGTTGACCAGAATGGAATCATCTCC 4317
            || ||||| ||||| |||||||||||||||||||||| ||||| |||||||||||||||
SBJCT: 4207 CTTATGTATTTTGTTGATGCCACCATGATCCGGAAGGTCGACCAAAATGGAATCATCTCC 4266

QUERY: 4318 ACCCTGCTGGGCTCCAATGACCTCACTGCCGTCCGGCCGCTGAGCTGTGATTCCAGCATG 4377
            ||||||||||||||||||||||||| || ||||| || ||||||||||| || ||||||
SBJCT: 4267 ACCCTGCTGGGCTCCAATGACCTCACAGCTGTCCGACCACTGAGCTGTGACTCTAGCATG 4326

QUERY: 4378 GATGTAGCCCAGGTTCGTCTGGAGTGGCCAACAGACCTTGCTGTCAATCCCATGGATAAC 4437
            || || |||||||| ||||| || ||||| ||||||||||| ||||| |||||||| ||
SBJCT: 4327 GACGTGGCCCAGGTCCGTCTAGAATGGCCGACAGACCTTGCGGTCAACCCCATGGACAAT 4386

QUERY: 4438 TCCTTGTATGTTCTAGAGAACAATGTCATCCTTCGAATCACCGAGAACCACCAAGTCAGC 4497
            ||| |||| || || |||||||| ||||||| || ||||||||||| ||||| ||||||
SBJCT: 4387 TCCCTGTACGTCCTGGAGAACAACGTCATCCTGCGGATCACCGAGAATCACCAGGTCAGC 4446

QUERY: 4498 ATCATTGCGGGACGCCCCATGCACTGCCAAGTTCCTGGCATTGACTACTCACTCAGCAAA 4557
            ||||| |||||||| |||||||||||||| ||||| ||||| |||||||| ||||||||
SBJCT: 4447 ATCATCGCGGGACGGCCCATGCACTGCCAGGTTCCCGGCATCGACTACTCGCTCAGCAAG 4506

QUERY: 4558 CTAGCCATTCACTCTGCCCTGGAGTCAGCCAGTGCCATTGCCATTTCTCACACTGGGGTC 4617
            || ||||| |||||||| ||||||||||||| ||||| |||||||||||||| |||||
SBJCT: 4507 CTCGCCATCCACTCTGCTCTGGAGTCAGCCAGCGCCATCGCCATTTCTCACACCGGGGTG 4566

QUERY: 4618 CTCTACATCACTGAGACAGATGAGAAGAAGATTAACCGTCTACGCCAGGTAACAACCAAC 4677
            ||||||||||| ||||| || ||||||||||| ||||| ||||||||||| || ||||||
SBJCT: 4567 CTCTACATCACCGAGACGGACGAGAAGAAGATCAACCGCCTACGCCAGGTCACCACCAAC 4626

QUERY: 4678 GGGGAGATCTGCCTTTTAGCTGGGGCAGCCTCGGACTGCGACTGCAAAAACGATGTCAAT 4737
            || ||||||||||| ||||| ||||||||||| ||||| ||||||||||| || |||||
SBJCT: 4627 GGAGAGATCTGCCTCTTAGCCGGGGCAGCCTCAGACTGTGACTGCAAAAATGACGTCAAC 4686

QUERY: 4738 TGCAACTGCTATTCAGGAGATGATGCCTACGCGACTGATGCCATCTTGAATTCCCCATCA 4797
            |||| ||||||||| |||||||| || ||||| || ||||||||||||||| ||||| ||
SBJCT: 4687 TGCATCTGCTATTCGGGAGATGACGCATACGCCACGGATGCCATCTTGAACTCCCCGTCC 4746

QUERY: 4798 TCCTTAGCTGTAGCTCCAGATGGTACCATTTACATTGCAGACCTTGGAAATATTCGGATC 4857
            ||||||||||| ||||| ||||| ||||| ||||| |||||||| || ||||| ||||||
SBJCT: 4747 TCCTTAGCTGTGGCTCCGGATGGCACCATCTACATCGCAGACCTCGGGAATATCCGGATC 4806

QUERY: 4858 AGGGCGGTCAGCAAGAACAAGCCTGTTCTTAATGCCTTCAACCAGTATGAGGCTGCATCC 4917
            |||||||||||||| ||||| ||||||||||| || |||||||||||||||||||| ||
SBJCT: 4807 AGGGCGGTCAGCAAAAACAAACCTGTTCTTAACGCGTTCAACCAGTATGAGGCTGCGTCT 4866

QUERY: 4918 CCCGGAGAGCAGGAGTTATATGTTTTCAACGCTGATGGCATCCACCAATACACTGTGAGC 4977
            || ||||| |||||   | || || |||||||| ||||| ||||| || ||||| ||||||
SBJCT: 4867 CCGGGAGAACAGGAACTGTACGTGTTCAACGCCGATGGTATCCATCAGTACACCGTGAGC 4926

QUERY: 4978 CTGGTGACAGGGGAGTACTTGTACAATTTCACATATAGTACTGACAATGATGTCACTGAA 5037
            |||||||| ||||||||||| ||||||||||| || ||   |||||||||||||||| ||
SBJCT: 4927 CTGGTGACCGGGGAGTACTTATACAATTTCACCTACAGCGCTGACAATGATGTCACCGAG 4986

QUERY: 5038 TTGATTGACAATAATGGGAATTCCCTGAAGATCCGTCGGGACAGCAGTGGCATGCCCCGT 5097
            ||||||||||| || ||||||||||| |||||||| |||||||||||||||||||||||
SBJCT: 4987 TTGATTGACAACAACGGGAATTCCCTAAAGATCCGCCGGGACAGCAGTGGCATGCCCCGA 5046
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QUERY: 5098 CACCTGCTCATGCCTGACAACCAGATCATCACCCTCACCGTGGGCACCAATGGAGGCCTC 5157
            ||||||||||||||||| || |||||||||||||| || ||||||||||| |||||||||
SBJCT: 5047 CACCTGCTCATGCCTGATAATCAGATCATCACCCTTACGGTGGGCACCAACGGAGGCCTC 5106

QUERY: 5158 AAAGTCGTGTCCACACAGAACCTGGAGCTTGGTCTCATGACCTATGATGGCAACACTGGG 5217
            |||| |||||| || ||||||||||||| || |||||||| |||||||| ||||||||
SBJCT: 5107 AAAGCCGTGTCAACGCAGAACCTGGAGCTGGCCTCATGACTTATGATGGGAACACTGGA 5166

QUERY: 5218 CTCCTGGCCACCAAGAGCGATGAAACAGGATGGACGACTTTCTATGACTATGACCACGAA 5277
            ||||| |||||||||||||||||||| |||||||| ||||| |||||||||||||||||
SBJCT: 5167 CTCCTAGCCACCAAGAGCGATGAAACCGGATGGACAACTTTTTATGACTATGACCACGAG 5226

QUERY: 5278 GGCCGCCTGACCAACGTGACGCGCCCCACGGGGGTGGTAACCAGTCTGCACCGGGAAATG 5337
            ||||| |||||||| ||||| ||||||||||||||||| ||||| |||||||||||||||
SBJCT: 5227 GGCCGTCTGACCAATGTGACTCGCCCCACGGGGGTGGTGACCAGCCTGCACCGGGAAATG 5286

QUERY: 5338 GAGAAATCTATTACCATTGACATTGAGAACTCCAACCGTGATGATGACGTCACTGTCATC 5397
            |||||||| || ||| |||||||||||||||||||||||||| | || |||||||| ||
SBJCT: 5287 GAGAAATCCATCACCGTTGACATTGAGAACTCCAACCGTGATAACGATGTCACTGTGATT 5346

QUERY: 5398 ACCAACCTCTCTTCAGTAGAGGCCTCCTACACAGTGGTACAAGATCAAGTTCGGAACAGC 5457
            ||||||||||||||||| |||||||||||||| ||||||||||||||||| |||||||||
SBJCT: 5347 ACCAACCTCTCTTCAGTGGAGGCCTCCTACACCGTGGTACAAGATCAAGTGCGGAACAGC 5406

QUERY: 5458 TACCAGCTCTGTAATAATGGTACCCTGAGGGTGATGTATGCTAATGGGATGGGTATCAGC 5517
            ||||||||||| |  || || |||||| | || ||||| || || || |||||  |||||
SBJCT: 5407 TACCAGCTCTGCAGCAACGGGACCCTGCGCGTCATGTACGCCAACGGCATGGGCGTCAGC 5466

QUERY: 5518 TTCCACAGCGAGCCCCATGTCCTAGCGGGCACCATCACCCCCACCATTGGACGCTGCAAC 5577
            ||||||||||||||||| ||||| || |||||| ||||||||||||| || ||||| |||
SBJCT: 5467 TTCCACAGCGAGCCCCACGTCCTCGCAGGCACCCTCACCCCCACCATCGGGCGCTGTAAC 5526

QUERY: 5578 ATCTCCCTGCCTATGGAGAATGGCTTAAACTCCATTGAGTGGCGCCTAAGAAAGGAACAG 5637
            ||||||||||| |||||||| ||| | |||||||| ||||||||||| || |||||||||
SBJCT: 5527 ATCTCCCTGCCCATGGAGAACGGCCTGAACTCCATCGAGTGGCGCCTGAGGAAGGAACAG 5586

QUERY: 5638 ATTAAAGGCAAAGTCACCATCTTTGGCAGGAAGCTCCGGGTCCATGGAAGAAATCTCTTG 5697
            |||||||||||||||||||||||||| |||||||| |||||||| ||||| || ||| ||
SBJCT: 5587 ATTAAAGGCAAAGTCACCATCTTTGGGAGGAAGCTTCGGGTCCACGGAAGGAACCTCCTG 5646

QUERY: 5698 TCCATTGACTATGATCGAAATATTCGGACTGAAAAGATCTATGATGACCACCGGAAGTTC 5757
            |||||||| ||||| |||||||| || ||||| ||||||||||| |||||||||||||||
SBJCT: 5647 TCCATTGATTATGACCGAAATATCCGCACTGAGAAGATCTATGACGACCACCGGAAGTTC 5706

QUERY: 5758 ACCCTGAGGATCATTTATGACCAGGTGGGCCGCCCCTTCCTCTGGCTGCCCAGCAGCGGG 5817
            ||||||||||||||||||||||||||||||||||||||||| ||||| |||||||| ||
SBJCT: 5707 ACCCTGAGGATCATTTATGACCAGGTGGGCCGCCCCTTCCTGTGGCTCCCCAGCAGTGGA 5766

QUERY: 5818 CTGGCAGCTGTCAACGTGTCATACTTCTTCAATGGGCGCCTGGCTGGGCTTCAGCGTGGG 5877
            ||||| || ||||| || || ||||||||||| ||||||||||| || || ||||| |||
SBJCT: 5767 CTGGCGGCCGTCAATGTCTCCTACTTCTTCAACGGGCGCCTGGCCGGCCTCCAGCGCGGG 5826

QUERY: 5878 GCCATGAGCGAGAGGACAGACATCGACAAGCAAGGCCGCATCGTGTCCCGCATGTTCGCT 5937
            ||||||||||||||||||||||| |||||||||||||| || |||||||| ||||||||
SBJCT: 5827 GCCATGAGCGAGAGGACAGACATTGACAAGCAAGGCCGGATTGTGTCCCGAATGTTCGCC 5886

QUERY: 5938 GACGGGAAAGTGTGGAGCTACTCCTACCTTGACAAGTCCATGGTCCTCCTGCTTCAGAGC 5997
            ||||||||||| |||||||| |||||||||||||||||||||||||||||||| ||||||
SBJCT: 5887 GACGGGAAAGTCTGGAGCTATTCCTACCTTGACAAGTCCATGGTCCTCCTGCTGCAGAGC 5946

QUERY: 5998 CAACGTCAGTATATATTTGAGTATGACTCCTCTGACCGCCTCCTTGCCGTCACCATGCCC 6057
            || |||||||| |||||||| ||||||||||||||||||||||  || ||||||||||||
SBJCT: 5947 CAGCGTCAGTACATATTTGAATATGACTCCTCTGACCGCCTCCACGCAGTCACCATGCCC 6006

QUERY: 6058 AGCGTGGCCCGGCACAGCATGTCCACACACACCTCCATCGGCTACATCCGTAATATTTAC 6117
            || || |||||||||||||||||||| ||||||||||| ||||||||||| || ||||||
SBJCT: 6007 AGTGTCGCCCGGCACAGCATGTCCACGCACACCTCCATTGGCTACATCCGGAACATTTAC 6066
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QUERY: 6118 AACCCGCCTGAAAGCAATGCTTCGGTCATCTTTGACTACAGTGATGACGGCCGCATCCTG 6177
SBJCT: 6067 AACCCACCGGAAAGCAACGCCTCGGTCATCTTTGACTACAGTGATGACGGCCGCATCCTG 6126

QUERY: 6178 AAGACCTCCTTTTTGGGCACCGGACGCCAGGTGTTCTACAAGTATGGGAAACTCTCCAAG 6237
SBJCT: 6127 AAGACGTCTTTCCTGGGCACCGGGCGCCAGGTGTTCTATAAGTACGGAAAACTGTCCAAG 6186

QUERY: 6238 TTATCAGAGATTGTCTACGACAGTACCGCCGTCACCTTCGGGTATGACGAGACCACTGGT 6297
SBJCT: 6187 TTATCGGAGATCGTCTACGACAGCACTGCCGTCACCTTCGGCTATGACGAGACCACTGGC 6246

QUERY: 6298 GTCTTGAAGATGGTCAACCTCCAAAGTGGGGGCTTCTCCTGCACCATCAGGTACCGGAAG 6357
SBJCT: 6247 GTCCTGAAGATGGTGAATCTCCAAAGCGGGGGCTTCTCCTGTACCATCAGGTACCGAAAG 6306

QUERY: 6358 ATTGGCCCCCTGGTGGACAAGCAGATCTACAGGTTCTCCGAGGAAGGCATGGTCAATGCC 6417
SBJCT: 6307 GTCGGGCCCCTCGTGGACAAGCAGATTTACAGGTTCTCTGAGGAAGGCATGATCAACGCC 6366

QUERY: 6418 AGGTTTGACTACACCTATCATGACAACAGCTTCCGCATCGCAAGCATCAAGCCCGTCATA 6477
SBJCT: 6367 AGGTTCGATTACACCTACCACGACAACAGCTTCCGCATCGCCAGCATCAAGCCCGTCATC 6426

QUERY: 6478 AGTGAGACTCCCCTCCCCGTTGACCTCTACCGCTATGATGAGATTTCTGGCAAGGTGGAA 6537
SBJCT: 6427 AGTGAGACTCCCCTTCCCGTTGACCTCTACCGCTACGATGAGATTTCTGGCAAGGTGGAA 6486

QUERY: 6538 CACTTTGGTAAGTTTGGAGTCATCTATTATGACATCAACCAGATCATCACCACTGCCGTG 6597
SBJCT: 6487 CACTTCGGCAAGTTCGGGGTCATCTACTACGACATCAACCAGATCATCACCACTGCCGTC 6546

QUERY: 6598 ATGACCCTCAGCAAACACTTCGACACCCATGGGCGGATCAAGGAGGTCCAGTATGAGATG 6657
SBJCT: 6547 ATGACACTCAGCAAGCACTTTGACACCCATGGGCGCATCAAGGAAGTGCAGTATGAGATG 6606

QUERY: 6658 TTCCGGTCCCTCATGTACTGGATGACGGTGCAATATGACAGCATGGGCAGGGTGATCAAG 6717
SBJCT: 6607 TTCCGGTCCCTCATGTACTGGATGACGGTGCAATATGACAGTATGGGCAGGGTCATCAAG 6666

QUERY: 6718 AGGGAGCTAAAACTGGGGCCCTATGCCAATACCACGAAGTACACCTATGACTACGATGGG 6777
SBJCT: 6667 AGGGAACTGAAACTGGGGCCCTATGCCAACACCACAAAGTACACCTATGACTACGACGGG 6726

QUERY: 6778 GACGGGCAGCTCCAGAGCGTGGCCGTCAATGACCGCCCGACCTGGCGCTACAGCTATGAC 6837
SBJCT: 6727 GACGGCCAGCTCCAGAGTGTGGCCGTCAATGACCGGCCTACCTGGCGTTATAGCTATGAC 6786

QUERY: 6838 CTTAATGGGAATCTCCACTTACTGAACCCAGGCAACAGTGTGCGCCTCATGCCCTTGCGC 6897
SBJCT: 6787 CTCAATGGGAACCTGCACCTGCTAAACCCAGGAAACAGTGCTCGCCTCATGCCGTTACGC 6846

QUERY: 6898 TATGACCTCCGGGATCGGATAACCAGACTCGGGGATGTGCAGTACAAAATTGACGACGAT 6957
SBJCT: 6847 TATGACCTCCGTGACCGGATAACCAGGCTAGGGGACGTGCAGTACAAAATCGATGATGAT 6906

QUERY: 6958 GGCTATCTGTGCCAGAGAGGGTCTGACATCTTCGAATACAATTCCAAGGGCCTCCTAACA 7017
SBJCT: 6907 GGCTATTTATGCCAGAGAGGATCTGACATCTTTGAATACAACTCCAAGGGCCTTCTAACG 6966

QUERY: 7018 AGAGCCTACAACAAGGCCAGCGGGTGGAGTGTCCAGTACCGCTATGATGGCGTAGGACGG 7077
SBJCT: 6967 AGAGCGTACAACAAGGCCAGCGGGTGGAGTGTGCAGTACCGCTATGATGGCGTGAGCCGC 7026

QUERY: 7078 CGGGCTTCCTACAAGACCAACCTGGGCCACCACCTGCAGTACTTCTACTCTGACCTCCAC 7137
SBJCT: 7027 CGGGCTTCCTACAAGACCAACCTGGGCCACCACCTACAGTACTTCTATTCCGACCTCCAC 7086
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QUERY: 7138 AACCCGACGCGCATCACCCATGTCTACAATCACTCCAACTCGGAGATTACCTCACTGTAC 7197
SBJCT: 7087 CACCCCACACGTATCACCCATGTTTACAACCACTCCAACTCTGAGATCACCTCACTCTAC 7146

QUERY: 7198 TACGACCTCCAGGGCCACCTCTTTGCCATGGAGAGCAGCAGTGGGGAGGAGTACTATGTT 7257
SBJCT: 7147 TATGACCTCCAGGGCCACCTCTTTGCCATGGAGAGCAGTAGTGGGGAAGAGTACTATGTT 7206

QUERY: 7258 GCCTCTGATAACACAGGGACTCCTCTGGCTGTGTTCAGCATCAACGGCCTCATGATCAAA 7317
SBJCT: 7207 GCCTCAGATAACACCGGGACTCCTCTGGCTGTTTTAGTATCAATGGCCTCATGATCAAG 7266

QUERY: 7318 CAGCTGCAGTACACGGCCTATGGGGAGATTTATTATGACTCCAACCCCGACTTCCAGATG 7377
SBJCT: 7267 CAACTCCAATACACAGCCTATGGGGAGATTTACTATGACTCCAATCCAGACTTTCAGATG 7326

QUERY: 7378 GTCATTGGCTTCCATGGGGGACTCTATGACCCCCTGACCAAGCTGGTCCACTTCACTCAG 7437
SBJCT: 7327 GTCATCGGCTTCCACGGAGGCCTCTACGACCCCCTCACCAAGCTCGTTCACTTTACGCAG 7386

QUERY: 7438 CGTGATTATGATGTGCTGGCAGGACGATGGACCTCCCCAGACTATACCATGTGGAAAAAC 7497
SBJCT: 7387 CGTGATTATGACGTGCTGGCAGGACGGTGGACGTCCCCCGACTACACCATGTGGAGGAAT 7446

QUERY: 7498 GTGGGCAAGGAGCCGGCCCCCTTTAACCTGTATATGTTCAAGAGCAACAATCCTCTCAGC 7557
SBJCT: 7447 GTGGGCAAGGAGCCAGCCCCCTTCAACCTGTACATGTTCAAGAACAACAATCCACTCAGT 7506

QUERY: 7558 AGTGAGCTAGATTTGAAGAACTACGTGACAGATGTGAAAAGCTGGCTTGTGATGTTTGGA 7617
SBJCT: 7507 AATGAGCTGGATTTAAAGAACTACGTGACAGACGTGAAGAGCTGGCTCGTGATGTTTGGA 7566

QUERY: 7618 TTTCAGCTTAGCAACATCATTCCTGGCTTCCCGAGAGCCAAAATGTATTTCGTGCCTCCT 7677
SBJCT: 7567 TTTCAGCTCAGCAACATCATTCCTGGATTCCCAAGAGCCAAAATGTATTTTGTGCCTCCC 7626

QUERY: 7678 CCCTATGAATTGTCAGAGAGTCAAGCAAGTGAGAATGGACAGCTCATTACAGGTGTCCAA 7737
SBJCT: 7627 CCCTATGAACTGTCAGAGAGCCAAGCAAGTGAGAATGGACAGCTCATTACAGGTGTCCAG 7686

QUERY: 7738 CAGACAACAGAGAGACATAACCAGGCCTTCATGGCTCTGGAAGGACAGGTCATTACTAAA 7797
SBJCT: 7687 CAGACAACAGAGAGGCATAACCAGGCCTTTCTGGCTCTAGAAGGACAGGTCATCTCTAAA 7746

QUERY: 7798 AAGCTCCACGCCAGCATCCGAGAGAAAGCAGGTCACTGGTTTGCCACCACCACGCCCATC 7857
SBJCT: 7747 AAGCTCCATGCAGGCATCCGAGAGAAAGCAGGCCACTGGTTTGCTACGACCACGCCCATC 7806

QUERY: 7858 ATTGGCAAAGGCATCATGTTTGCCATCAAAGAAGGGCGGGTGACCACGGGCGTGTCCAGC 7917
SBJCT: 7807 ATCGGCAAAGGCATCATGTTCGCCATCAAAGAAGGGCGGGTGACCACAGGCGTGTCTAGC 7866

QUERY: 7918 ATCGCCAGCGAAGATAGCCGCAAGGTGGCATCTGTGCTGAACAACGCCTACTACCTGGAC 7977
SBJCT: 7867 ATCGCCAGTGAGGACAGCCGCAAGGTAGCATCCGTGTTGAACAACGCCTACTACTTGGAC 7926

QUERY: 7978 AAGATGCACTACAGCATCGAGGGCAAGGACACCCACTACTTTGTGAAGATTGGCTCAGCC 8037
SBJCT: 7927 AAGATGCACTACAGCATCGAGGGCAAGGACACACACTACTTCGTGAAGATCGGTGCAGCG 7986

QUERY: 8038 GATGGCGACCTGGTCACACTAGGCACCACCATCGGCCGCAAGGTGCTAGAGAGCGGGGTG 8097
SBJCT: 7987 GACGGTGACCTGGTTACGCTGGGGACCACCATTGGGCGCAAGGTGCTGGAGAGCGGGGTG 8046

QUERY: 8098 AACGTGACCGTGTCCCAGCCCACGCTGCTGGTCAACGGCAGGACTCGAAGGTTCACGAAC 8157
SBJCT: 8047 AACGTGACCGTGTCACAGCCCACGCTGCTGGTGAACGGCAGGACTCGAAGGTTCACCAAC 8106

QUERY: 8158 ATTGAGTTCCAGTACTCCACGCTGCTGCTCAGCATCCGCTATGGCCTCACCCCCGACACC 8217
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SBJCT: 8107 ATTGAATTCCAGTACTCCACGCTGCTGCTCAGCATACGCTACGGCCTCACCCCCGACACA 8166

QUERY: 8218 CTGGACGAAGAGAAGGCCCGCGTCCTGGACCAGGCGAGACAGAGGGCCCTGGGCACGGCC 8277
            ||||| ||||||||||||||||||||||||||| ||| ||||||||||||||||||| || |||
SBJCT: 8167 CTGGATGAAGAGAAGGCCCGCGTCCTGGACCAAGCGCGACAGAGGGCCCTGGGTACTGCC 8226

QUERY: 8278 TGGGCCAAGGAGCAGCAGAAAGCCAGGGACGGGAGAGGGGAGCCGCCTGTGGACTGAG 8337
            ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||| |||
SBJCT: 8227 TGGGCCAAGGAGCAGCAGAAAGCCAGGGACGGGAGAGGGCAGCCGTCTGTGGACGGAG 8286

QUERY: 8338 GGCGAGAAGCAGCAGCTTCTGAGCACCGGGCGCGTGCAAGGGTACGAGGGATATTACGTG 8397
            |||||||||||||| || |||||||| || || |||||||| || ||||| |||||||||
SBJCT: 8287 GGCGAGAAGCAGCAACTCCTGAGCACGGGACGGGTGCAAGGTTATGAGGGCTATTACGTG 8346

QUERY: 8398 CTTCCCGTGGAGCAATACCCAGAGCTTGCAGACAGTAGCAGCAACATCCAGTTTTTAAGA 8457
            ||||| ||||| || |||||||||||| ||||||||||||||||||||||||| ||||||
SBJCT: 8347 CTTCCGGTGGAACAGTACCCAGAGCTGGCAGACAGTAGCAGCAACATCCAGTTCTTAAGA 8406

QUERY: 8458 CAGAATGAGATGGAAAGAGGTAACAAAATAATCTGCTGCCATTCCTTGTCTGAATGGCT 8517
            ||||||||||||||||||||||||||||||| ||||||||||   ||| ||||  |||||
SBJCT: 8407 CAGAATGAGATGGAAAGAGGTAACAAAATAACCTGCTGCCACCTCTTCTCTGGGTGGCT 8466

QUERY: 8518 CAGCAGGAGTAACTGTTATCTCCTCTCCTAAGGAGATGAAGACCTAACAGGGGCACTGCG 8577
            ||||||||| |||||| | |||||||||||||||||| |||||||||||||||||||| |
SBJCT: 8467 CAGCAGGAGCAACTGTGACCTCCTCTCCTAAGGAGACGAAGACCTAACAGGGGCACTGAG 8526

QUERY: 8578 GCTGGGCTGCTTTAGGAGACCAAGTGGCAAGAAAGCTCACATTTTTGAGTTCAAATGCT 8637
            || ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
SBJCT: 8527 GCCGGGCTGCTTTAGGACCCCAAGTGGCAAGAAAGCTCACATTTTTGAGTTCAAATGCT 8586

QUERY: 8638 ACTGTCCAAGCGAGAAGTCCCTCATCCTGAAGTAGACTAAAGCCCGGCTGAAAATTCCGA 8697
            ||||||||||||  ||||||||||||||||||||||||| ||| ||||   |||||| ||
SBJCT: 8587 ACTGTCCAAGCGCAAAGTCCCTCATCCTGAAGTAGACTAGAGCTCGGCCACAAATTCTGA 8646

QUERY: 8698 GGAAAACAAAAC 8709
            ||||||||||||
SBJCT: 8647 GGAAAACAAAAC 8658

SCORE = 1459 BITS (736), EXPECT = 0.0
 IDENTITIES = 1081/1196 (90%)
 STRAND = PLUS / PLUS

QUERY: 270   ATCTGGAATAATGGATGTAAAGGACCGGCGACACCGCTCTTTGACCAGAGGACGCTGTGG 329
             ||||| |||||||||||| ||||| |||||||| |||||||||||||| ||||| |||||
SBJCT: 123   ATCTGCAATAATGGATGTGAAGGATCGGCGACATCGCTCTTTGACCAGGGGACGGTGTGG 182

QUERY: 330   CAAAGAGTGTCGCTACACAAGCTCCTCTCTGGACAGTGAGGACTGCCGGGTGCCCACACA 389
             ||| |||||||||||||| |||||||||||||||||||||||||||||| ||||||| ||
SBJCT: 183   CAAGGAGTGTCGCTACACCAGCTCCTCTCTGGACAGTGAGGACTGCCGTGTGCCCACGCA 242

QUERY: 390   GAAATCCTACAGCTCCAGTGAGACTCTGAAGGCCTATGACCATGACAGCAGGATGCACTA 449
             ||| |||||||| |||||||||||| |||||||| ||||||||||||||||| ||||||||
SBJCT: 243   GAAGTCCTACAGTTCCAGTGAGACCCTGAAGGCTTATGACCATGACAGCAGAATGCACTA 302

QUERY: 450   TGGAAACCGAGTCACAGACCTCATCCACCGGGAGTCAGATGAGTTTCCTAGACAAGGAAC 509
             |||||||||||||||||||||  | |||||||||||| |||||||||| |||||||||  |
SBJCT: 303   TGGAAACCGAGTCACAGACCTGGTGCACCGGGAGTCCGATGAGTTTTCTAGACAAGGGGC 362

QUERY: 510   CAACTTCACCCTTGCCGAACTGGGCATCTGTGAGCCCTCCCCACACCGAAGCGGCTACTG 569
              || |||||||| || ||| |||| ||||| |||||||||||||||||||| || |||||
SBJCT: 363   TAATTTCACCCTGGCAGAATTGGGAATCTGCGAGCCCTCCCCACACCGAAGTGGTTACTG 422

QUERY: 570   CTCCGACATGGGGATCCTTCACCAGGGCTACTCCCTTAGCACAGGGTCTGACGCCGACTC 629
              ||||||||||||||||| |||||||||||||||||| ||||| ||||||||| || |||||
SBJCT: 423   TTCCGACATGGGGATCCTCCACCAGGGCTACTCCCTGAGCACTGGGTCTGATGCGGACTC 482

QUERY: 630   CGACACCGAGGAGGGATGTCTCCAGAACACGCCATCAGACTGTGGGGCAGAGGGATAAA 689
              ||||||||||||||||||||||||||| |||||||||||||||||  ||||||||||
SBJCT: 483   GGACACCGAGGAGGGATGTCTCCAGAACATGCCATCAGACTGTGGGGACGAGGGATAAA 542
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QUERY: 690    ATCCAGGCGCAGTTCCGGCCTGTCCAGTCGTGAAAACTCGGCCCTTACCCTGACTGACTC 749
              ||| |||||||| || ||| ||||||| || || ||||| |||||||| |||||||| ||
SBJCT: 543    ATCGAGGCGCAGCTCTGGCTTGTCCAGCCGCGAGAACTCAGCCCTTACTCTGACTGATTC 602

QUERY: 750    TGACAACGAAAACAAATCAGATGATGAGAACGGTCGTCCCATTCCACCTACATCCTCGCC 809
              |||||| ||||| ||||| ||||| || || ||||| ||||||||||||||||||||| |
SBJCT: 603    TGACAATGAAAATAAATCGGATGACGACAATGGTCGACCCATTCCACCTACATCCTCGTC 662

QUERY: 810    TAGTCTCCTCCCATCTGCTCAGCTGCCTAGCTCCCATAATCCTCCACCAGTTAGCTGCCA 869
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 663    TAGCCTCCTCCCATCTGCTCAGCTGCCTAGCTCCCATAATCCTCCACCAGTTAGCTGCCA 722

QUERY: 870    GATGCCATTGCTAGACAGCAACACCTCCCATCAAATCATGGACACCAACCCTGATGAGGA 929
              ||||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||
SBJCT: 723    GATGCCATTGCTAGACAGCAACACCTCCCATCAGATCATGGACACCAACCCCGATGAGGA 782

QUERY: 930    ATTCTCCCCCAATTCATACCTGCTCAGAGCATGCTCAGGGCCCCAGCAAGCCTCCAGCAG 989
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||| ||
SBJCT: 783    ATTCTCCCCTAATTCATACCTGCTCAGAGCATGCTCAGGGCCCCAGCAAGCCTCCAGTAG 842

QUERY: 990    TGGCCCTCCGAACCACCACAGCCAGTCGACTCTGAGGCCCCCTCTCCCACCCCCTCACAA 1049
              ||||||||||||||||||||||||||| || |||||||||||||| ||||| ||||| ||
SBJCT: 843    TGGCCCTCCGAACCACCACAGCCAGTCAACGCTGAGGCCCCCTCTGCCACCTCCTCATAA 902

QUERY: 1050   CCACACGCTGTCCCATCACCACTCGTCCGCCAACTCCCTCAACAGGAACTCACTGACCAA 1109
              |||||| |||||||| |||||||| || ||||||||||||||||| ||||||||||||||
SBJCT: 903    CCACACCCTGTCCCACCACCACTCCTCTGCCAACTCCCTCAACAGAAACTCACTGACCAA 962

QUERY: 1110   TCGGCGGAGTCAGATCCACGCCCCGGCCCCAGCGCCCAATGACCTGGCCACCACACCAGA 1169
              |||||||||||| ||||||||||| || || || |||||||||||||||||||| || ||
SBJCT: 963    TCGGCGGAGTCAAATCCACGCCCCAGCTCCTGCACCCAATGACCTGGCCACCACGCCGGA 1022

QUERY: 1170   GTCCGTTCAGCTTCAGGACAGCTGGGTGCTAAACAGCAACGTGCCACTGGAGACCCGGCA 1229
              |||||||||||| ||||||||||||||||| ||||| |||||||| |||||||| |||||
SBJCT: 1023   GTCCGTTCAGCTCCAGGACAGCTGGGTGCTGAACAGTAACGTGCCGCTGGAGACGCGGCA 1082

QUERY: 1230   CTTCCTCTTCAAGACCTCCTCGGGGAGCACACCCTTGTTCAGCAGCTCTTCCCCGGGATA 1289
              ||||||||||||||| ||||| || ||||||||| |||||||||||||||| || |||||
SBJCT: 1083   CTTCCTCTTCAAGACGTCCTCCGGAAGCACACCCCTGTTCAGCAGCTCTTCTCCAGGATA 1142

QUERY: 1290   CCCTTTGACCTCAGGAACGGTTTACACGCCCCCGCCCCGCCTGCTGCCCAGGAATACTTT 1349
              ||| ||||||||||| || ||||| || || || ||||||||||||||  ||||||| ||
SBJCT: 1143   CCCCTTGACCTCAGGGACCGTTTATACACCACCACCCCGCCTGCTGCCACGGAATACATT 1202

QUERY: 1350   CTCCAGGAAGGCTTTCAAGCTGAAGAAGCCCTCCAAATACTGCAGCTGGAAATGTGCTGC 1409
              ||| |||||||| |||||||||||||| ||||||||||||||||| |||||||| || ||
SBJCT: 1203   CTCTAGGAAGGCCTTCAAGCTGAAGAAACCCTCCAAATACTGCAGTTGGAAATGCGCCGC 1262

QUERY: 1410   CCTCTCCGCCATTGCCGCGGCCCTCCTCTTGGCTATTTTGCTGGCGTATTTCATAG 1465
              ||| || ||||||||||| ||||||||  |||| ||||||||||| ||||||||||
SBJCT: 1263   CCTGTCTGCCATTGCCGCTGCCCTCCTTCTGGCCATTTTGCTGGCCTATTTCATAG 1318

SCORE = 1427 BITS (720), EXPECT = 0.0
 IDENTITIES = 996/1088 (91%)
 STRAND = PLUS / PLUS

QUERY: 1464   AGTGCCCTGGTCGTTGAAAAACAGCAGCATAGACAGTGGTGAAGCAGAAGTTGGTCGGCG 1523
              |||||||||||||||||||||||||||||||||||| || || |||||||| ||||| ||
SBJCT: 1440   AGTGCCCTGGTCGTTGAAAAACAGCAGCATAGACAGCGGCGAGGCAGAAGTCGGTCGACG 1499

QUERY: 1524   GGTAACACAAGAAGTCCCACCAGGGGTGTTTTGGAGGTCACAAATTCACATCAGTCAGCC 1583
              ||| ||||| ||||||||||||||||||||||||||||| || |||||||||||||||||
SBJCT: 1500   GGTGACACAGGAAGTCCCACCAGGGGTGTTTTGGAGGTCCCAGATTCACATCAGTCAGCC 1559

QUERY: 1584   CCAGTTCTTAAAGTTCAACATCTCCCTCGGGAAGGACGCTCTCTTTGGTGTTTACATAAG 1643
               |||||||||||||||||||||||||| |||||||| || ||||| || || ||||||||
SBJCT: 1560   TCAGTTCTTAAAGTTCAACATCTCCCTGGGGAAGGATGCCCTCTTCGGCGTCTACATAAG 1619

QUERY: 1644   AAGAGGACTTCCACCATCTCATGCCCAGTATGACTTCATGGAACGTCTGGACGGGAAGGA 1703
              ||||||||| |||||||||||||| |||||||||||||||||||| |||||||| |||||
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SBJCT: 1620 AAGAGGACTGCCACCATCTCATGCACAGTATGACTTCATGGAACGCCTGGACGGAAAGGA 1679

QUERY: 1704 GAAGTGGAGTGTGGTTGAGTCTCCCAGGGAACGCCGGAGCATACAGACCTTGGTTCAGAA 1763
            ||||||||||||||| ||||| |||||||||||||||||||| |||||| |||| |||||
SBJCT: 1680 GAAGTGGAGTGTGGTCGAGTCACCCAGGGAACGCCGGAGCATCCAGACCCTGGTGCAGAA 1739

QUERY: 1764 TGAAGCCGTGTTTGTGCAGTACCTGGATGTGGGCCTGTGGCATCTGGCCTTCTACAATGA 1823
             || || ||||| ||||||||| ||||||||||||||||||| || ||||||||||||||
SBJCT: 1740 CGAGGCTGTGTTCGTGCAGTACTTGGATGTGGGCCTGTGGCACCTCGCCTTCTACAATGA 1799

QUERY: 1824 TGGAAAAGACAAAGAGATGGTTTCCTTCAATACTGTTGTCCTAGATTCAGTGCAGGACTG 1883
             || || ||||| |||||||| ||||||||||| |||||| |||||||||||||||||||
SBJCT: 1800 CGGCAAGGACAAGGAGATGGTCTCCTTCAATACGGTTGTCTTAGATTCAGTGCAGGACTG 1859

QUERY: 1884 TCCACGTAACTGCCATGGGAATGGTGAATGTGTGTCCGGGGTGTGTCACTGTTTCCCAGG 1943
            |||||| |||||||| ||||| || ||||| ||||| ||  |||||||||||||||||||
SBJCT: 1860 TCCACGAAACTGCCACGGGAACGGCGAATGCGTGTCTGGACTGTGTCACTGTTTCCCAGG 1919

QUERY: 1944 ATTTCTAGGAGCAGACTGTGCTAAAGCTGCCTGCCCTGTCCTGTGCAGTGGGAATGGACA 2003
            ||| ||||| |||||||| |||||||||||||||||||| ||||||||||||||||||||
SBJCT: 1920 ATTCCTAGGTGCAGACTGCGCTAAAGCTGCCTGCCCTGTTCTGTGCAGTGGGAATGGACA 1979

QUERY: 2004 ATATTCTAAAGGGACGTGCCAGTGCTACAGCGGCTGGAAAGGTGCAGAGTGCGACGTGCC 2063
             ||||| |||||||| |||||||||||||| ||||||||||| ||||| ||||| |||||
SBJCT: 1980 GTATTCCAAAGGGACATGCCAGTGCTACAGTGGCTGGAAAGGAGCAGAATGCGATGTGCC 2039

QUERY: 2064 CATGAATCAGTGCATCGATCCTTCCTGCGGGGGCCACGGCTCCTGCATTGATGGGAACTG 2123
            |||||| |||||||||||||||||||| ||||||||||||||||||||||||||||||||
SBJCT: 2040 CATGAACCAGTGCATCGATCCTTCCTGTGGGGGCCACGGCTCCTGCATTGATGGGAACTG 2099

QUERY: 2124 TGTCTGCTCTGCTGGCTACAAAGGCGAGCACTGTGAGGAAGTTGATTGCTTGGATCCCAC 2183
             || ||  | ||||||||||| ||||||||||| || ||||| |||||||||||||| ||
SBJCT: 2100 CGTGTGTGCAGCTGGCTACAAGGGCGAGCACTGCGAAGAAGTGGATTGCTTGGATCCAAC 2159

QUERY: 2184 CTGCTCCAGCCACGGAGTCTGTGTGAATGGAGAATGCCTGTGCAGCCCTGGCTGGGGTGG 2243
            |||||||||||| || ||||||||||| ||||| || || |||||||| |||||||| ||
SBJCT: 2160 CTGCTCCAGCCATGGTGTCTGTGTGAACGGAGAGTGTCTATGCAGCCCCGGCTGGGGCGG 2219

QUERY: 2244 TCTGAACTGTGAGCTGGCGAGGGTCCAGTGCCCAGACCAGTGCAGTGGGCATGGCACGTA 2303
             || ||||| |||||||||||||||||||||||||||||||| |||||||||||||| ||
SBJCT: 2220 GCTCAACTGCGAGCTGGCGAGGGTCCAGTGCCCAGACCAGTGTAGTGGGCATGGCACTTA 2279

QUERY: 2304 CCTGCCTGACACGGGCCTCTGCAGCTGCGATCCCAACTGGATGGGTCCCGACTGCTCTGT 2363
            ||| |||||| | |||||||||| ||| ||||| || |||||||||||||||||||||||
SBJCT: 2280 CCTCCCTGACTCTGGCCTCTGCAACTGTGATCCGAATTGGATGGGTCCCGACTGCTCTGT 2339

QUERY: 2364 TGAAGTGTGCTCAGTAGACTGTGGCACTCACGGCGTCTGCATCGGGGGAGCCTGCCGCTG 2423
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2340 TGAAGTGTGCTCAGTAGACTGTGGCACTCACGGCGTCTGCATCGGGGGAGCCTGCCGCTG 2399

QUERY: 2424 TGAAGAGGGCTGGACAGGCGCAGCGTGTGACCAGCGCGTGTGCCACCCCCGCTGCATTGA 2483
            ||||||||||||||||||||| || |||||||||||||||||||||||||||||||||||
SBJCT: 2400 TGAAGAGGGCTGGACAGGCGCGGCTTGTGACCAGCGCGTGTGCCACCCCCGCTGCATTGA 2459

QUERY: 2484 GCACGGGACCTGTAAAGATGGCAAATGTGAATGCCGAGAGGGCTGGAATGGTGAACACTG 2543
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2460 GCACGGGACCTGTAAAGATGGCAAATGTGAATGCCGAGAGGGCTGGAATGGTGAACACTG 2519

QUERY: 2544 CACCATTG 2551
            ||||||||
SBJCT: 2520 CACCATTG 2527
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In this search it was also found that the FCTR3bcd and e nucleic acid had homology to six fragments of *Gallus gallus* partial mRNA for teneurin-2. It has 2780 of 3449 bases (80%) identical to bases 3386-6834, 1553 of 1862 bases (83%) identical to bases 1414-3275, 540 of

628 bases (85%) identical to bases 587-1214, 593 of 725 bases (81%) identical to bases 7084-7808, 429 of 515 bases (83%) identical to bases 7895-8409, and 397 of 475 bases (83%) identical to bases 20-494 of *Gallus gallus* partial mRNA for teneurin-2. (EMBL Acc: GGA278031) (Table 3O).

Table 3O. BLASTN of FCTR3b, c, d, and e against *Gallus gallus* Teneurin-2 mRNA (SEQ ID NO:67)

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>GI|10241573|EMB|AJ279031.1|GGA279031 GALLUS GALLUS PARTIAL MRNA FOR TENEURIN-2 (TEN2
GENE), LONG SPLICE
            VARIANT
          LENGTH = 8409

 SCORE = 1532 BITS (773), EXPECT = 0.0
 IDENTITIES = 2780/3449 (80%)
 STRAND = PLUS / PLUS

QUERY: 3458 TGATGGTGGCTGTCGAGGGGCATCTCTTCCAGAAGTCATTCCAGGCTTCTCCCAACCTGG 3517
            ||||||| || || || |||||||| || || || ||||| | ||| ||||||||| |||
SBJCT: 3386 TGATGGTAGCAGTAGAAGGGCATCTATTTCAAAATCATTTCTGGCATCTCCCAACTTGG 3445

QUERY: 3518 CCTCCACCTTCATCTGGGACAAGACAGATGCGTATGGCCAAAGGGTGTATGGACTCTCAG 3577
            | |  || |||||||||||||| |||||||| ||||| || | ||| |||||  | ||||
SBJCT: 3446 CTTATACATTCATCTGGGACAAAACAGATGCATATGGTCAGAAGGTTTATGGGTTGTCAG 3505

QUERY: 3578 ATGCTGTTGTGTCTGTCGGGTTTGAATATGAGACCTGTCCCAGTCTAATTCTCTGGGAGA 3637
            ||||||| || ||||| || |||||||||||||| ||||||||| | ||||| |||||||
SBJCT: 3506 ATGCTGTAGTTTCTGTGGGTTTTGAATATGAGACTTGTCCCAGTTTGATTCTGTGGGAGA 3565

QUERY: 3638 AAAGGACAGCCCTCCTTCAGGGATTCGAGCTGGACCCCTCCAACCTCGGTGGCTGGTCCC 3697
            ||||||| || || || || ||||| ||||| || || ||||| || || || |||||
SBJCT: 3566 AAAGGACTGCGCTGCTGCAAGGATTTGAGCTAGATCCTTCCAATCTAGGAGGATGGTCTT 3625

QUERY: 3698 TAGACAAACACCACATCCTCAATGTTAAAAGTGGAATCCTACACAAAGGCACTGGGGAAA 3757
            | || ||||| ||  | || ||||| || ||||| ||  | |||||||||| ||| ||||
SBJCT: 3626 TGGATAAACATCATGTACTGAATGTCAAGAGTGGTATATTGCACAAAGGCAATGGAGAAA 3685

QUERY: 3758 ACCAGTTCCTGACCCAGCAGCCTGCCATCATCACCAGCATCATGGGCAATGGTCGCCGCC 3817
            | ||||| || || |||||||| ||  | || |||||||| ||||| ||||| |||||
SBJCT: 3686 ATCAGTTTCTAACTCAGCAGCCAGCTGTGATAACCAGCATTATGGGGAATGGGCGCCGAA 3745

QUERY: 3818 GGAGCATTTCCTGTCCCAGCTGCAACGGCCTTGCTGAAGGCAACAAGCTGCTGGCCCCAG 3877
            | ||||| |||||||| |||||||| || ||||| ||||| || |||||  ||||||| |
SBJCT: 3746 GAAGCATATCCTGTCCTAGCTGCAATGGTCTTGCAGAAGGAAATAAGCTTTTGGCCCCTG 3805

QUERY: 3878 TGGCTCTGGCTGTTGGAATCGATGGGAGCCTCTATGTGGGTGACTTCAATTACATCCGAC 3937
            | || ||||| || ||||| ||||| ||||||| ||| || || || |||||||| || |
SBJCT: 3806 TAGCACTGGCAGTGGGAATTGATGGAAGCCTCTTTGTTGGAGATTTTAATTACATTCGGC 3865

QUERY: 3938 GCATCTTTCCCTCTCGAAATGTGACCAGCATCTTGGAGTTACGAAATAAAGAGTTTAAAC 3997
            | ||||| || ||  | |||||||| ||||| |||||| |  ||||||||||||||||||
SBJCT: 3866 GTATCTTCCCATCCAGGAATGTGACTAGCATATTGGAGCTGAGAAATAAAGAGTTTAAAC 3925

QUERY: 3998 ATAGCAACAACCCAGCACACAAGTACTACTTGGCAGTGGACCCCGTGTCCGGCTCGCTCT 4057
            |||||||||| || || ||||| |||||  |||| ||||||||||| || ||||| || |
SBJCT: 3926 ATAGCAACAATCCTGCTCACAAATACTATCTGGCCGTGGACCCCGTTTCGGGCTCCCTGT 3985

QUERY: 4058 ACGTGTCCGACACCAACAGCAGGAGAATCTACCGCGTCAAGTCTCTGAGTGGAACCAAAG 4117
            |||| || |||||||||||| |  | || |||   ||||| ||||| | ||| || ||||
SBJCT: 3986 ACGTATCAGACACCAACAGCCGACGGATATACAAAGTCAAATCTCTTACTGGCACGAAAG 4045

QUERY: 4118 ACCTGGCTGGGAATTCGGAAGTTGTGGCAGGGACGGGAGAGCAGTGTCTACCCTTTGATG 4177
            |||||||||| ||||| ||||| || || ||||| |||||||| || || ||||||||||
SBJCT: 4046 ACCTGGCTGGTAATTCTGAAGTGGTAGCGGGGACTGGAGAGCAATGCCTGCCCTTTGATG 4105
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QUERY: 4178 AAGCCCGCTGCGGGGATGGAGGGAAGGCCATAGATGCAACCCTGATGAGCCCGAGAGGTA 4237

SBJCT: 4106 AAGCCAGATGTGGAGATGGAGGGAAAGCAGTGGACGCAACCCTAATGAGTCCTCGAGGAA 4165

QUERY: 4238 TTGCAGTAGACAAGAATGGGCTCATGTACTTTGTCGATGCCACCATGATCCGGAAGGTTG 4297

SBJCT: 4166 TTGCAGTGGATAAGTATGGACTCATGTATTTTGTTGATGCCACTATGATTCGAAAAGTGG 4225

QUERY: 4298 ACCAGAATGGAATCATCTCCACCCTGCTGGGCTCCAATGACCTCACTGCCGTCCGGCCGC 4357

SBJCT: 4226 ATCAGAATGGAATTATATCAACTCTGCTGGGCTCCAATGACCTAACTGCCGTCCGACCTC 4285

QUERY: 4358 TGAGCTGTGATTCCAGCATGGATGTAGCCCAGGTTCGTCTGGAGTGGCCAACAGACCTTG 4417

SBJCT: 4286 TAAGCTGTGATTCCAGCATGGATGTCAGCCAGGTACGGCTGGAGTGGCCTACTGATCTCG 4345

QUERY: 4418 CTGTCAATCCCATGGATAACTCCTTGTATGTTCTAGAGAACAATGTCATCCTTCGAATCA 4477

SBJCT: 4346 CTGTCGATCCCATGGACAACTCACTTTATGTCCTAGAGAACAATGTTATTTTACGGATCA 4405

QUERY: 4478 CCGAGAACCACCAAGTCAGCATCATTGCGGGACGCCCCATGCACTGCCAAGTTCCTGGCA 4537

SBJCT: 4406 CAGAAAACCATCAAGTTAGCATTATTGCTGGACGCCCCATGCACTGCCAGGTTCCTGGTA 4465

QUERY: 4538 TTGACTACTCACTCAGCAAACTAGCCATTCACTCTGCCCTGGAGTCAGCCAGTGCCATTG 4597

SBJCT: 4466 TAGACTACTCTCTTAGCAAACTGGCTATTCATTCCGCACTTGAATCAGCCAGTGCCATTG 4525

QUERY: 4598 CCATTTCTCACACTGGGGTCCTCTACATCACTGAGACAGATGAGAAGAAGATTAACCGTC 4657

SBJCT: 4526 CCATCTCACACACAGGAGTTCTTTACATCAGTGAGACAGATGAAAAAAAAATTAATCGGC 4585

QUERY: 4658 TACGCCAGGTAACAACCAACGGGGAGATCTGCCTTTTAGCTGGGGCAGCCTCGGACTGCG 4717

SBJCT: 4586 TACGCCAGGTAACTACCAATGGAGAAATATGCCTTCTTGCAGGGGCAGCTTCAGACTGTG 4645

QUERY: 4718 ACTGCAAAAACGATGTCAATTGCAACTGCTATTCAGGAGATGATGCCTACGCGACTGATG 4777

SBJCT: 4646 ATTGCAAAAATGATGTCAACTGTAATTGCTATTCTGGGGATGATGGGTATGCCACTGATG 4705

QUERY: 4778 CCATCTTGAATTCCCCATCATCCTTAGCTGTAGCTCCAGATGGTACCATTTACATTGCAG 4837

SBJCT: 4706 CCATCTTAAATTCACCATCTTCCTTAGCTGTGGCCCCAGATGGTACCATCTACATAGCTG 4765

QUERY: 4838 ACCTTGGAAATATTCGGATCAGGGCGGTCAGCAAGAACAAGCCTGTTCTTAATGCCTTCA 4897

SBJCT: 4766 ATCTCGGAAATATCCGCATTAGGGCTGTCAGTAAAAACAGGCCCATTCTTAATTCTTTTA 4825

QUERY: 4898 ACCAGTATGAGGCTGCATCCCCCGGAGAGCAGGAGTTATATGTTTTCAACGCTGATGGCA 4957

SBJCT: 4826 ACCAATATGAAGCTGCATCTCCAGGAGAACAGGAGCTGTATGTCTTCAATGCTGATGGGA 4885

QUERY: 4958 TCCACCAATACACTGTGAGCCTGGTGACAGGGGAGTACTTGTACAATTTCACATATAGTA 5017

SBJCT: 4886 TTCACCAGTACACTCTCAGCCTTGTTACCGGGGAGTACTTGTACAATTTCACCTATAGCA 4945

QUERY: 5018 CTGACAATGATGTCACTGAATTGATTGACAATAATGGGAATTCCCTGAAGATCCGTCGGG 5077

SBJCT: 4946 GTGATAACGATGTCACCGAGGTGATGGACAGCAATGGCAACTCCTTGAAGGTCCGTCGGG 5005

QUERY: 5078 ACAGCAGTGGCATGCCCCGTCACCTGCTCATGCCTGACAACCAGATCATCACCCTCACCG 5137

SBJCT: 5006 ATGCCAGCGGAATGCCCCGCCATTTACTGATGCCTGATAATCAGATTGTCACGCTGGCCG 5065

QUERY: 5138 TGGGCACCAATGGAGGCCTCAAAGTCGTGTCCACACAGAACCTGGAGCTTGGTCTCATGA 5197

SBJCT: 5066 TTGGCACTAATGGTGGACTCAAACTAGTCTCAACGCAGACCCTGGAACTTGGATTAATGA 5125

QUERY: 5198 CCTATGATGGCAACACTGGGCTCCTGGCCACCAAGAGCGATGAAACAGGATGGACGACTT 5257
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SBJCT: 5126 CTTATAACGGAAACAGTGGTCTCTTAGCAACGAAGAGTGATGAAACAGGATGGACAACAT 5185

QUERY: 5258 TCTATGACTATGACCACGAAGGCCGCCTGACCAACGTGACGCGCCCCACGGGGGTGGTAA 5317
SBJCT: 5186 TTTATGACTATGATCATGAAGGGCGCCTGACCAATGTAACACGTCCCACTGGAGTGGTAA 5245

QUERY: 5318 CCAGTCTGCACCGGGAAATGGAGAAATCTATTACCATTGACATTGAGAACTCCAACCGTG 5377
SBJCT: 5246 CTAGCCTTCATCGAGAAATGGAAAAGTCTATTACCATCGACATTGAGAATTCTAATCGGG 5305

QUERY: 5378 ATGATGACGTCACTGTCATCACCAACCTCTCTTCAGTAGAGGCCTCCTACACAGTGGTAC 5437
SBJCT: 5306 ATGATGATGTCACGGTCATCACAAATCTCTCCTCTGTGGAGGCTTCCTATACAGTTGTTC 5365

QUERY: 5438 AAGATCAAGTTCGGAACAGCTACCAGCTCTGTAATAATGGTACCCTGAGGGTGATGTATG 5497
SBJCT: 5366 AAGATCAAGTGAGGAACAGCTACCAGCTCTGTAATAATGGTACTTTGAGAGTGATGTATG 5425

QUERY: 5498 CTAATGGGATGGGTATCAGCTTCCACAGCGAGCCCCATGTCCTAGCGGGCACCATCACCC 5557
SBJCT: 5426 CCAATGGCATGAGTATTAGCTTTCACAGCGAACCTCATGTCCTGGCTGGGACAGTAACTC 5485

QUERY: 5558 CCACCATTGGACGCTGCAACATCTCCCTGCCTATGGAGAATGGCTTAAACTCCATTGAGT 5617
SBJCT: 5486 CCACCATAGGACGATGTAATATTTCTCTACCAATGGAGAATGGTTTGAACTCAATTGAAT 5545

QUERY: 5618 GGCGCCTAAGAAAGGAACAGATTAAAGGCAAAGTCACCATCTTTGGCAGGAAGCTCCGGG 5677
SBJCT: 5546 GGCGTCTGAGGAAAGAACAGATTAAAGGCAAAGTGACTGTGTTTGGAAGAAAGCTCAGGG 5605

QUERY: 5678 TCCATGGAAGAAATCTCTTGTCCATTGACTATGATCGAAATATTCGGACTGAAAAGATCT 5737
SBJCT: 5606 TTCATGGAAGGAATTTGCTGTCCATTGATTACGACCGGAATATACGCACAGAAAAAATCT 5665

QUERY: 5738 ATGATGACCACCGGAAGTTCACCCTGAGGATCATTTATGACCAGGTGGGCCGCCCCTTCC 5797
SBJCT: 5666 ACGATGATCACCGCAAGTTCACCCTGAGGATAATTTACGATCAGCTGGGACGGCCCTTCC 5725

QUERY: 5798 TCTGGCTGCCCAGCAGCGGGCTGGCAGCTGTCAACGTGTCATACTTCTTCAATGGGCGCC 5857
SBJCT: 5726 TCTGGCTGCCCAGCAGCGGCCTGGCTGCCGTCAACGTGTCCTATTTCTTCAACGGGCGCC 5785

QUERY: 5858 TGGCTGGGCTTCAGCGTGGGGCCATGAGCGAGAGGACAGACATCGACAAGCAAGGCCGCA 5917
SBJCT: 5786 TGGCTGGGCTTCAGCGCGGAGCCATGAGCGAAAGGACAGACATCGACAAGCAAGGCAGGA 5845

QUERY: 5918 TCGTGTCCCGCATGTTCGCTGACGGGAAAGTGTGGAGCTACTCCTACCTTGACAAGTCCA 5977
SBJCT: 5846 TCATATCGCGCATGTTTGCAGATGGGAAGGTTTGGAGTTACACCTACCTAGAAAAATCCA 5905

QUERY: 5978 TGGTCCTCCTGCTTCAGAGCCAACGTCAGTATATATTTGAGTATGACTCCTCTGACCGCC 6037
SBJCT: 5906 TGGTACTACTGCTTCAGAGCCAGCGGCAGTACATCTTTGAGTATGATTCTTCAGACCGGC 5965

QUERY: 6038 TCCTTGCCGTCACCATGCCCAGCGTGGCCCGGCACAGCATGTCCACACACACCTCCATCG 6097
SBJCT: 5966 TCCATGCTGTTACTATGCCTAGTGTTGCTCGGCATAGCATGTCAACTCACACGTCTGTTG 6025

QUERY: 6098 GCTACATCCGTAATATTTACAACCCGCCTGAAAGCAATGCTTCGGTCATCTTTGACTACA 6157
SBJCT: 6026 GCTACATTAGGAATATTTATAATCCTCCTGAAAGCAACGCATCAGTGATTTTTGATTACA 6085

QUERY: 6158 GTGATGACGGCCGCATCCTGAAGACCTCCTTTTTGGGCACCGGACGCCAGGTGTTCTACA 6217
SBJCT: 6086 GTGATGATGGGAGGATTTTGAAAACATCATTTTTAGGTACTGGTCGACAAGTCTTTTACA 6145

QUERY: 6218 AGTATGGGAAACTCTCCAAGTTATCAGAGATTGTCTACGACAGTACCGCCGTCACCTTCG 6277
SBJCT: 6146 AGTATGGAAAGCTATCCAAATTATCTGAAATTGTTTATGACAGTACTGCGGTTACTTTTG 6205
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QUERY: 6278 GGTATGACGAGACCACTGGTGTCTTGAAGATGGTCAACCTCCAAAGTGGGGGCTTCTCCT 6337
            | ||||| || || || |||||| | || ||||| ||  | |||||||| || || || |
SBJCT: 6206 GATATGATGAAACTACAGGTGTCCTAAAAATGGTGAATTTGCAAAGTGGAGGATTTTCTT 6265

QUERY: 6338 GCACCATCAGGTACCGGAAGATTGGCCCCCTGGTGGACAAGCAGATCTACAGGTTCTCCG 6397
            | || ||| | || || || |||||||| || || ||||| || |||||||| ||||| |
SBJCT: 6266 GTACAATCCGCTATCGTAAAATTGGCCCTCTTGTTGACAAACAAATCTACAGATTCTCTG 6325

QUERY: 6398 AGGAAGGCATGGTCAATGCCAGGTTTGACTACACCTATCATGACAACAGCTTCCGCATCG 6457
            | ||||| ||||||||||| |||||||| || || ||||| ||||| || || ||||| |
SBJCT: 6326 AAGAAGGTATGGTCAATGCAAGGTTTGATTATACATATCACGACAATAGTTTTCGCATTG 6385

QUERY: 6458 CAAGCATCAAGCCCGTCATAAGTGAGACTCCCCTCCCCGTTGACCTCTACCGCTATGATG 6517
            |||||||||| ||| ||||||||||||||| || || ||||| || ||||| |||||||
SBJCT: 6386 CAAGCATCAAACCCATCATAAGTGAGACTCCTCTTCCAGTTGATCTTTACCGTTATGATG 6445

QUERY: 6518 AGATTTCTGGCAAGGTGGAACACTTTGGTAAGTTTGGAGTCATCTATTATGACATCAACC 6577
            ||||||||||||| || || || ||||| || |||||||| || |||||||| || || |
SBJCT: 6446 AGATTTCTGGCAAAGTTGAGCATTTTGGCAAATTTGGAGTTATTTATTATGATATAAATC 6505

QUERY: 6578 AGATCATCACCACTGCCGTGATGACCCTCAGCAAACACTTCGACACCCATGGGCGGATCA 6637
            | || || || || || || ||||| || || || ||||| || ||||| || || || |
SBJCT: 6506 AAATTATTACTACAGCAGTTATGACACTGAGTAAGCACTTTGATACCCACGGACGCATTA 6565

QUERY: 6638 AGGAGGTCCAGTATGAGATGTTCCGGTCCCTCATGTACTGGATGACGGTGCAATATGACA 6697
            | || || || |||||||||||||| ||||| |||||||||||||| |||||||||||||
SBJCT: 6566 AAGAAGTTCAATATGAGATGTTCCGATCCCTGATGTACTGGATGACTGTGCAATATGACA 6625

QUERY: 6698 GCATGGGCAGGGTGATCAAGAGGGAGCTAAAACTGGGGCCCTATGCCAATACCACGAAGT 6757
            ||||||| || || |  || || || || ||||| ||||| |||||||| || || ||||
SBJCT: 6626 GCATGGGAAGAGTAACTAAAAGAGAACTGAAACTTGGGCCGTATGCCAACACAACCAAGT 6685

QUERY: 6758 ACACCTATGACTACGATGGGGACGGCAGCTCCAGAGCGTGGCCGTCAATGACCGCCCCGA 6817
            | |||||||| || ||||| || |||||  | || ||||| || || |||||  | || |
SBJCT: 6686 ATACCTATGATTATGATGGAGATGGCAATTGCAAAGCGTAGCAGTAAATGATAGGCCTA 6745

QUERY: 6818 CCTGGCGCTACAGCTATGACCTTAATGGGAATCTCCACTTACTGAACCCAGGCAACAGTG 6877
            ||||||| ||||| |||||||| ||||| ||||| ||| | ||||| || || |||||||
SBJCT: 6746 CCTGGCGTTACAGTTATGACCTGAATGGAAATCTTCACCTCCTGAATCCTGGAAACAGTG 6805

QUERY: 6878 TGCGCCTCATGCCCTTGCGCTATGACCTC 6906
            | ||  | |||||| ||||||| ||||||
SBJCT: 6806 TTCGATTGATGCCCCTGCGCTACGACCTC 6834
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SCORE = 1241 BITS (626), EXPECT = 0.0
IDENTITIES = 1553/1862 (83%)
STRAND = PLUS / PLUS

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QUERY: 1486 AGCAGCATAGACAGTGGTGAAGCAGAAGTTGGTCGGCGGGTAACACAAGAAGTCCCACCA 1545
            ||||||||||| ||||| ||| |||||||||| ||   ||| || ||||| || || ||
SBJCT: 1414 AGCAGCATAGATAGTGGAGAAACAGAAGTTGGCCGCAAGGTCACCCAAGAGGTGCCCCCT 1473

QUERY: 1546 GGGGTGTTTTGGAGGTCACAAATTCACATCAGTCAGCCCCAGTTCTTAAAGTTCAACATC 1605
            || ||||| ||| |||| || || || ||||| ||||| |||||| | |||||||||||
SBJCT: 1474 GGAGTGTTCTGGCGGTCTCAGATCCATATCAGCCAGCCACAGTTCCTGAAGTTCAACATA 1533

QUERY: 1606 TCCCTCGGGAAGGACGCTCTCTTTGGTGTTTACATAAGAAGAGGACTTCCACCATCTCAT 1665
            ||||| |||||||| ||||| || |||||||| |||||||||||||| |||||||| |||
SBJCT: 1534 TCCCTAGGGAAGGATGCTCTTTTCGGTGTTTATATAAGAAGAGGACTCCCACCATCACAT 1593

QUERY: 1666 GCCCAGTATGACTTCATGGAACGTCTGGACGGGAAGGAGAAGTGGAGTGTGGTTGAGTCT 1725
            || |||||||| |||||||||||  |||| ||||| ||||| ||||||||||| || ||
SBJCT: 1594 GCACAGTATGATTTCATGGAACGCTTGGATGGGAAAGAGAAATGGAGTGTGGTGGAATCC 1653

QUERY: 1726 CCCAGGGAACGCCGGAGCATACAGACCTTGGTTCAGAATGAAGCCGTGTTTGTGCAGTAC 1785
            ||  ||||||| || || || |||||  | ||||||||||| || |||||||| ||||||
SBJCT: 1654 CCACGGGAACGGCGAAGTATTCAGACTCTTGTTCAGAATGAGGCTGTGTTTGTTCAGTAC 1713

QUERY: 1786 CTGGATGTGGGCCTGTGGCATCTGGCCTTCTACAATGATGGAAAAGACAAAGAGATGGTT 1845
             ||||||||||  ||||||| ||||| || ||||||||||| || ||||||||  ||||
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SBJCT: 1714 TTGGATGTGGGTTTGTGGCACCTGGCGTTTTACAATGATGGCAAGGACAAAGAAGTGGTC 1773

QUERY: 1846 TCCTTCAATACTGTTGTCCTAGATTCAGTGCAGGACTGTCCACGTAACTGCCATGGGAAT 1905
            ||||||| ||| ||| |  | ||||||||||| |||||||||||||| || ||||| |||
SBJCT: 1774 TCCTTCAGTACAGTTATTTTGGATTCAGTGCAAGACTGTCCACGTAATTGTCATGGCAAT 1833

QUERY: 1906 GGTGAATGTGTGTCCGGGGTGTGTCACTGTTTCCCAGGATTTCTAGGAGCAGACTGTGCT 1965
            || || ||||| || || || || |||||||| || |||||||  |||||||| ||||||
SBJCT: 1834 GGCGAGTGTGTTTCTGGTGTCTGCCACTGTTTTCCCGGATTTCATGGAGCAGATTGTGCT 1893

QUERY: 1966 AAAGCTGCCTGCCCTGTCCTGTGCAGTGGGAATGGACAATATTCTAAAGGGACGTGCCAG 2025
            |||||||||||||| || ||||||||||| ||||| || || || ||||| || |||  |
SBJCT: 1894 AAAGCTGCCTGCCCGGTGCTGTGCAGTGGCAATGGTCAGTACTCCAAAGGAACCTGCTTG 1953

QUERY: 2026 TGCTACAGCGGCTGGAAAGGTGCAGAGTGCGACGTGCCCATGAATCAGTGCATCGATCCT 2085
            |||||||| |||||||||||| | || || || || ||||| |  ||||| || |||||
SBJCT: 1954 TGCTACAGTGGCTGGAAAGGTCCGGAATGTGATGTACCCATCAGCCAGTGTATTGATCCC 2013

QUERY: 2086 TCCTGCGGGGGCCACGGCTCCTGCATTGATGGGAACTGTGTCTGCTCTGCTGGCTACAAA 2145
            || || || || || || |||||||| || |||||||||||||| ||   |||||| |||
SBJCT: 2014 TCGTGTGGAGGTCATGGTTCCTGCATCGAAGGGAACTGTGTCTGTTCCATTGGCTATAAA 2073

QUERY: 2146 GGCGAGCACTGTGAGGAAGTTGATTGCTTGGATCCCACCTGCTCCAGCCACGGAGTCTGT 2205
            || ||  |||||||||||||||||||||| ||||| || |||||||  ||||| ||||||
SBJCT: 2074 GGAGAAAACTGTGAGGAAGTTGATTGCTTAGATCCAACATGCTCCAATCACGGGGTCTGT 2133

QUERY: 2206 GTGAATGGAGAATGCCTGTGCAGCCCTGGCTGGGGTGGTCTGAACTGTGAGCTGGCGAGG 2265
            ||||| |||||||| || |||||||| |||||||||||  | |||||||||||  | ||
SBJCT: 2134 GTGAACGGAGAATGTCTCTGCAGCCCAGGCTGGGGTGGAATAAACTGTGAGCTTCCCAGA 2193

QUERY: 2266 GTCCAGTGCCCAGACCAGTGCAGTGGGCATGGCACGTACCTGCCTGACACGGGCCTCTGC 2325
            | ||||||||||||||||||||||||||||||||| |||||| ||||||| || |||||
SBJCT: 2194 GCCCAGTGCCCAGACCAGTGCAGTGGGCATGGCACATACCTGTCTGACACCGGTCTCTGT 2253

QUERY: 2326 AGCTGCGATCCCAACTGGATGGGTCCCGACTGCTCTGTTGAAGTGTGCTCAGTAGACTGT 2385
            ||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
SBJCT: 2254 AGCTGCGATCCCAACTGGATGGGTCCCGACTGCTCCGTTGAAGTGTGCTCTGTAGACTGT 2313

QUERY: 2386 GGCACTCACGGCGTCTGCATCGGGGGAGCCTGCCGCTGTGAAGAGGGCTGGACAGGCGCA 2445
            ||||| || || || ||||| || ||||| || ||||||||||| || |||||||| |
SBJCT: 2314 GGCACCCATGGGGTGTGCATTGGCGGAGCGTGTCGCTGTGAAGAAGGGTGGACAGGAGTG 2373

QUERY: 2446 GCGTGTGACCAGCGCGTGTGCCACCCCCGCTGCATTGAGCACGGGACCTGTAAAGATGGC 2505
            |||||||||||||| ||||| || ||||| || |  |||||||| || |||||||||||
SBJCT: 2374 GCGTGTGACCAGCGTGTGTGTCATCCCCGGTGTACAGAGCACGGAACTTGTAAAGATGGG 2433

QUERY: 2506 AAATGTGAATGCCGAGAGGGCTGGAATGGTGAACACTGCACCATTGGTAGGCAAACGGCA 2565
            |||||||||||| |||||||||||||||| || |||||||||||||||||||||||| ||
SBJCT: 2434 AAATGTGAATGCAGAGAGGGCTGGAATGGGGAGCACTGCACCATTGGTAGGCAAACGACA 2493

QUERY: 2566 GGCACCGAAACAGATGGCTGCCCTGACTTGTGCAACGGTAACGGGAGATGCACACTGGGT 2625
            ||||||||||||||||||||||||||||||||||| || |||||||| ||||| |||||
SBJCT: 2494 GGCACCGAAACAGATGGCTGCCCTGACTTGTGCAATGGCAACGGGAGGTGCACGCTGGGC 2553

QUERY: 2626 CAGAACAGCTGGCAGTGTGTCTGCCAGACCGGCTGGAGAGGGCCCGGATGCAACGTTGCC 2685
            |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
SBJCT: 2554 CAGAACAGCTGGCAGTGTGTCTGCCAGACCGGCTGGAGAGGGCCTGGATGCAACGTTGCC 2613

QUERY: 2686 ATGGAAACTTCCTGTGCTGATAACAAGGATAATGAGGGAGATGGCCTGGTGGATTGTTTG 2745
            |||||||| |||||||| |||||||||||||| |||||||||||| |||| || ||  |
SBJCT: 2614 ATGGAAACCTCCTGTGCCGATAACAAGGATAACGAGGGAGATGGCTTGGTTGACTGCCTA 2673

QUERY: 2746 GACCCTGACTGCTGCCTGCAGTCAGCCTGTCAGAACAGCCTGCTCTGCCGGGGGTCCCGG 2805
            | ||| || |||||||| |||||  | ||||| ||||||||||| |||||||| |||||
SBJCT: 2674 GTCCCAGATTGCTGCCTCCAGTCCACTTGTCAAAACAGCCTGCTGTGCCGGGGTTCCCGC 2733

QUERY: 2806 GACCCACTGGACATCATTCAGCAGGGCCAGACGGATTGGCCCGCAGTGAAGTCCTTCTAT 2865
            || || || |||||||| || ||| ||||  | | ||  || || |||||||| ||||||
SBJCT: 2734 GATCCTCTTGACATCATACAACAGAGCCATTCTGGTTCACCAGCTGTGAAGTCATTCTAT 2793
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QUERY: 2866 GACCGTATCAAGCTCTTGGCAGGCAAGGATAGCACCCACATCATTCCTGGAGAGAACCCT 2925
            || || ||||||||||| |  || ||||| ||||| || |||||||| ||||| || ||
SBJCT: 2794 GATCGAATCAAGCTCTTAGTGGGGAAGGACAGCACTCATATCATTCCAGGAGAAAATCCC 2853

QUERY: 2926 TTCAACAGCAGCTTGGTTTCTCTCATCCGAGGCCAAGTAGTAACTACAGATGGAACTCCC 2985
            |||||||||||| | || ||||| ||  |||||||||| || |||||||||||||| ||
SBJCT: 2854 TTCAACAGCAGCCTTGTGTCTCTTATAAGAGGCCAAGTGGTGACTACAGATGGAACGCCT 2913

QUERY: 2986 CTGGTCGGTGTGAACGTGTCTTTTGTCAAGTACCCAAAATACGGCTACACCATCACCCGC 3045
            || || || || |||||||| ||||||||||| ||||| || ||||| |||||||| ||
SBJCT: 2914 CTAGTTGGGGTCAACGTGTCATTTGTCAAGTATCCAAAGTATGGCTATACCATCACTCGT 2973

QUERY: 3046 CAGGATGGCACGTTCGACCTGATCGCAAATGGAGGTGCTTCCTTGACTCTACACTTTGAG 3105
            |||||||||| ||| ||| || | || || || ||  | ||| ||| | ||||||||
SBJCT: 2974 CAGGATGGCATGTTTGACTTGGTTGCTAACGGTGGATCATCCCTAACTTTGCACTTTGAA 3033

QUERY: 3106 CGAGCCCCGTTCATGAGCCAGGAGCGCACTGTGTGGCTGCCGTGGAACAGCTTTTACGCC 3165
            || ||||| || ||||| |||||  | || || |||||||||||||||||||| || |||
SBJCT: 3034 CGGGCCCCATTTATGAGTCAGGAAAGGACAGTATGGCTGCCGTGGAACAGCTTCTATGCC 3093

QUERY: 3166 ATGGACACCCTGGTGATGAAGACCGAGGAGAACTCCATCCCCAGCTGTGACCTCAGTGGC 3225
            |||||||| || || ||||| || |||||||||||||| ||||||||||| |||||||||
SBJCT: 3094 ATGGACACGCTTGTAATGAAAACAGAGGAGAACTCCATTCCCAGCTGTGATCTCAGTGGC 3153

QUERY: 3226 TTTGTCCGGCCTGATCCAATCATCATCTCCTCCCCACTGTCCACCTTCTTTAGTGCTGCC 3285
            |||||| | ||||||||| ||||||| || || |||||||| || ||||| |||| |||
SBJCT: 3154 TTTGTCAGACCTGATCCAGTCATCATTTCATCACCACTGTCAACTTTCTTCAGTGATGCT 3213

QUERY: 3286 CCTGGGCAGAATCCCATCGTGCCTGAGACCCAGGTTCTTCATGAAGAAATCGAGCTCCCT 3345
            ||||| |  ||||| || || || || ||||||||||||||||||||||| ||| |||||
SBJCT: 3214 CCTGGCCGAAATCCTATTGTACCAGAAACCCAGGTTCTTCATGAAGAAATTGAGGTCCCT 3273

QUERY: 3346 GG 3347
            ||
SBJCT: 3274 GG 3275

SCORE =  547 BITS (276), EXPECT = E-152
 IDENTITIES = 540/628 (85%)
 STRAND = PLUS / PLUS

QUERY: 782  GTCGTCCCATTCCACCTACATCCTCGCCTAGTCTCCTCCCATCTGCTCAGCTGCCTAGCT 841
            |||||||||||||||||||||||||| |||| || |||||||||||||||||||| || |
SBJCT: 587  GTCGTCCCATTCCACCTACATCCTCGTCTAGCCTTCTCCCATCTGCTCAGCTGCCCAGTT 646

QUERY: 842  CCCATAATCCTCCACCAGTTAGCTGCCAGATGCCATTGCTAGACAGCAACACCTCCCATC 901
            | ||||||||||||||||||||||||||||||||||||||||||||||| || |||||||
SBJCT: 647  CTCATAATCCTCCACCAGTTAGCTGCCAGATGCCATTGCTAGACAGCAATACGTCCCATC 706

QUERY: 902  AAATCATGGACACCAACCCTGATGAGGAATTCTCCCCCAATTCATACCTGCTCAGAGCAT 961
            |||||||||||||||| ||||| ||||| ||||| || ||||||||||| || |||||||
SBJCT: 707  AAATCATGGACACCAATCCTGACGAGGAGTTCTCTCCTAATTCATACCTACTAAGAGCAT 766

QUERY: 962  GCTCAGGGCCCCAGCAAGCCTCCAGCAGTGGCCCTCCGAACCACCACAGCCAGTCGACTC 1021
            | |||||||| ||||| || ||||||||||||||| || ||||| ||||||||||| || |
SBJCT: 767  GTTCAGGGCCACAGCAGGCATCCAGCAGTGGCCCTTCAAACCATCACAGCCAGTCAACGC 826

QUERY: 1022 TGAGGCCCCCTCTCCCACCCCCTCACAACCACACGCTGTCCCATCACCACTCGTCCGCCA 1081
            ||||||| |||||||| || |||||||||||| ||||||||||||| |||||||| ||||
SBJCT: 827  TGAGGCCACCTCTCCCCCCTCCTCACAACCACTCGCTGTCCCATCATCACTCGTCTGCCA 886

QUERY: 1082 ACTCCCTCAACAGGAACTCACTGACCAATCGGCGGAGTCAGATCCACGCCCCGGCCCCAG 1141
            ||||||||||||||||||| || ||||| || || |  ||||||||||| || || || |
SBJCT: 887  ACTCCCTCAACAGGAACTCGCTCACCAACCGCCGCAACCAGATCCACGCGCCTGCTCCCG 946

QUERY: 1142 CGCCCAATGACCTGGCCACCACACCAGAGTCCGTTCAGCTTCAGGACAGCTGGGTGCTAA 1201
            | |||||||||||||| ||||| || ||||| || ||||| ||||||||||||||||| |
SBJCT: 947  CTCCCAATGACCTGGCGACCACGCCTGAGTCTGTGCAGCTGCAGGACAGCTGGGTGCTCA 1006

QUERY: 1202 ACAGCAACGTGCCACTGGAGACCCGGCACTTCCTCTTCAAGACCTCCTCGGGGAGCACAC 1261
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            ||||||||||||| ||||||||| |||| ||| | || ||||| || || || |  || |
SBJCT: 1007 ACAGCAACGTGCCGCTGGAGACCAGGCATTTCTTGTTTAAGACATCTTCTGGAACGACTC 1066

QUERY: 1262 CCTTGTTCAGCAGCTCTTCCCCGGGATACCCTTTGACCTCAGGAACGGTTTACACGCCCC 1321
            |  ||||||| ||||||||||| || |||||  ||||||||||||| ||||| || || |
SBJCT: 1067 CGCTGTTCAGTAGCTCTTCCCCTGGCTACCCACTGACCTCAGGAACAGTTTATACTCCAC 1126

QUERY: 1322 CGCCCCGCCTGCTGCCCAGGAATACTTTCTCCAGGAAGGCTTTCAAGCTGAAGAAGCCCT 1381
            | ||| | ||| | || || ||||| || |||||||| || ||||||||||| |||||||
SBJCT: 1127 CTCCCAGGCTGTTACCTAGAAATACATTTTCCAGGAATGCATTCAAGCTGAAAAAGCCCT 1186

QUERY: 1382 CCAAATACTGCAGCTGGAAATGTGCTGC 1409
            |||| || || |||||||||||||||||
SBJCT: 1187 CCAAGTATTGTAGCTGGAAATGTGCTGC 1214

SCORE =  391 BITS (197), EXPECT = E-105
 IDENTITIES = 593/725 (81%)
 STRAND = PLUS / PLUS

QUERY: 7156 CATGTCTACAATCACTCCAACTCGGAGATTACCTCACTGTACTACGACCTCCAGGGCCAC 7215
            |||||||||||||| ||||| || || |||||||| ||||| || || || || ||||||
SBJCT: 7084 CATGTCTACAATCATTCCAATTCAGAAATTACCTCTCTGTATTATGATCTGCAAGGCCAC 7143

QUERY: 7216 CTCTTTGCCATGGAGAGCAGCAGTGGGGAGGAGTACTATGTTGCCTCTGATAACACAGGG 7275
            |||||||| |||||||| ||||||||||| || || ||||| ||||| |||||||| || 
SBJCT: 7144 CTCTTTGCAATGGAGAGTAGCAGTGGGGAAGAATATTATGTCGCCTCCGATAACACGGGC 7203

QUERY: 7276 ACTCCTCTGGCTGTGTTCAGCATCAACGGCCTCATGATCAAACAGCTGCAGTACACGGCC 7335
            ||||| || || || ||||||||||| |||||||||||||||||||| |||||||| || 
SBJCT: 7204 ACTCCGCTAGCCGTATTCAGCATCAATGGCCTCATGATCAAACAGCTTCAGTACACTGCA 7263

QUERY: 7336 TATGGGGAGATTTATTATGACTCCAACCCCGACTTCCAGATGGTCATTGGCTTCCATGGG 7395
            || || ||||||||||||||||| ||||| || |||||| |||| ||||| |||||||| 
SBJCT: 7264 TACGGAGAGATTTATTATGACTCAAACCCTGATTTCCAGCTGGTTATTGGGTTCCATGGA 7323

QUERY: 7396 GGACTCTATGACCCCCTGACCAAGCTGGTCCACTTCACTCAGCGTGATTATGATGTGCTG 7455
            || || ||||| ||  | ||||| || ||||| || || ||  | || || ||||| || 
SBJCT: 7324 GGGCTGTATGATCCTTTAACCAAACTCGTCCATTTTACCCAAAGGGACTACGATGTCCTT 7383

QUERY: 7456 GCAGGACGATGGACCTCCCCAGACTATACCATGTGGAAAAACGTGGGCAAGGAGCCGGCC 7515
            || ||||| ||||| || || || || || |||||||||||| | || |  || || || 
SBJCT: 7384 GCTGGACGCTGGACATCTCCTGATTACACAATGTGGAAAAACATTGGTAGAGAACCTGCT 7443

QUERY: 7516 CCCTTTAACCTGTATATGTTCAAGAGCAACAATCCTCTCAGCAGTGAGCTAGATTTGAAG 7575
            ||||| || ||||| ||||||||||| ||||| |||||||||| ||| || ||| | |||
SBJCT: 7444 CCCTTCAATCTGTACATGTTCAAGAGTAACAACCCTCTCAGCAATGAACTGGATCTAAAG 7503

QUERY: 7576 AACTACGTGACAGATGTGAAAAGCTGGCTTGTGATGTTTGGATTTCAGCTTAGCAACATC 7635
            || || || |||||||| ||||||||||| |||||||| |||||||||||||||||||| 
SBJCT: 7504 AATTATGTAACAGATGTCAAAAGCTGGCTGGTGATGTTCGGATTTCAGCTTAGCAACATT 7563

QUERY: 7636 ATTCCTGGCTTCCCGAGAGCCAAAATGTATTTCGTGCCTCCTCCCTATGAATTGTCAGAG 7695
            |||||||||||||| ||||| |||||||| || ||| | ||||| || ||  || | |||
SBJCT: 7564 ATTCCTGGCTTCCCTAGAGCAAAAATGTACTTTGTGTCACCTCCATACGAGCTGACTGAG 7623

QUERY: 7696 AGTCAAGCAAGTGAGAATGGACAGCTCATTACAGGTGTCCAACAGACAACAGAGAGACAT 7755
            ||||||||  |||| ||||||||||| |||||||| ||||| ||||||||||| ||||| 
SBJCT: 7624 AGTCAAGCGTGTGAAAATGGACAGCTAATTACAGGAGTCCAGCAGACAACAGAAAGACAC 7683

QUERY: 7756 AACCAGGCCTTCATGGCTCTGGAAGGACAGGTCATTACTAAAAAGCTCCACGCCAGCATC 7815
            || || || ||||||||||| || |||||||||||  ||||||   | || ||||| || 
SBJCT: 7684 AATCAAGCTTTCATGGCTCTTGAGGGACAGGTCATATCTAAAAGATTACATGCCAGTATT 7743

QUERY: 7816 CGAGAGAAAGCAGGTCACTGGTTTGCCACCACCACGCCCATCATTGGCAAAGGCATCATG 7875
             |||| |||||||| ||||||||||| || | ||| || || ||||| ||||| ||||||
SBJCT: 7744 AGAGAAAAAGCAGGCCACTGGTTTGCAACAAGCACTCCTATTATTGGGAAAGGAATCATG 7803

QUERY: 7876 TTTGC 7880
            |||||
SBJCT: 7804 TTTGC 7808
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SCORE =  339 BITS (171), EXPECT = 2E-89
 IDENTITIES = 429/515 (83%)
 STRAND = PLUS / PLUS

QUERY: 7967 ACTACCTGGACAAGATGCACTACAGCATCGAGGGCAAGGACACCCACTACTTTGTGAAGA 8026
            |||||||||| || |||||||||||||||||||| ||||| || ||||||||||| ||||
SBJCT: 7895 ACTACCTGGAAAAAATGCACTACAGCATCGAGGGGAAGGATACTCACTACTTTGTCAAGA 7954

QUERY: 8027 TTGGCTCAGCCGATGGCGACCTGGTCACACTAGGCACCACCATCGGCCGCAAGGTGCTAG 8086
            | |||||||||||| ||||||| ||||| || |  |  |||| |||  | ||||| || |
SBJCT: 7955 TAGGCTCAGCCGATAGCGACCTCGTCACCCTCGCGATGACCAGCGGGAGGAAGGTCCTGG 8014

QUERY: 8087 AGAGCGGGGTGAACGTGACCGTGTCCCAGCCCACGCTGCTGGTCAACGGCAGGACTCGAA 8146
            | ||||| || ||||||||||| |||||||| || || ||  ||||||| |||||||||
SBJCT: 8015 ACAGCGGAGTAAACGTGACCGTCTCCCAGCCAACCCTCCTTATCAACGGAAGGACTCGAC 8074

QUERY: 8147 GGTTCACGAACATTGAGTTCCAGTACTCCACGCTGCTGCTCAGCATCCGCTATGGCCTCA 8206
            ||||||| ||||| ||||| ||||| ||||| |||||| ||| ||||||||| || ||||
SBJCT: 8075 GGTTCACAAACATCGAGTTTCAGTATTCCACCCTGCTGATCAACATCCGCTACGGGCTCA 8134

QUERY: 8207 CCCCCGACACCCTGGACGAAGAGAAGGCCCGCGTCCTGGACCAGGCGAGACAGAGGGCCC 8266
            || ||||||| ||||| || |||||||| || || || ||||||||  | ||| | ||||
SBJCT: 8135 CCGCCGACACGCTGGATGAGGAGAAGGCACGAGTGCTAGACCAGGCTCGGCAGCGAGCCC 8194

QUERY: 8267 TGGGCACGGCCTGGGCCAAGGAGCAGCAGAAAGCCAGGGACGGGAGAGAGGGGAGCCGCC 8326
            ||||  ||||||||||||| ||||||||||| ||  |||| ||  | ||||| ||||||
SBJCT: 8195 TGGGGTCGGCCTGGGCCAAAGAGCAGCAGAAGGCACGGGATGGCCGCGAGGGCAGCCGCG 8254

QUERY: 8327 TGTGGACTGAGGGCGAGAAGCAGCAGCTTCTGAGCACCGGGCGCGTGCAAGGGTACGAGG 8386
            | ||||| || || |||||||| |||||||||| ||| ||  | || ||||| |||||||
SBJCT: 8255 TATGGACAGACGGAGAGAAGCAACAGCTTCTGAACACGGGAAGGGTTCAAGGTTACGAGG 8314

QUERY: 8387 GATATTACGTGCTTCCCGTGGAGCAATACCCAGAGCTTGCAGACAGTAGCAGCAACATCC 8446
            ||||||| ||  | || |||||||| ||||||||||| ||||||||||||||||||||||
SBJCT: 8315 GATATTATGTCTTGCCTGTGGAGCAGTACCCAGAGCTAGCAGACAGTAGCAGCAACATCC 8374

QUERY: 8447 AGTTTTTAAGACAGAATGAGATGGGAAAGAGGTAA 8481
            ||||||||||||||||||| |||||||||||||||
SBJCT: 8375 AGTTTTTAAGACAGAATGAAATGGGAAAGAGGTAA 8409

 SCORE =  323 BITS (163), EXPECT = 1E-84
 IDENTITIES = 397/475 (83%)
 STRAND = PLUS / PLUS

QUERY: 299  GACACCGCTCTTTGACCAGAGGACGCTGTGGCAAAGAGTGTCGCTACACAAGCTCCTCTC 358
            |||||||||||||||| ||||| || || || || ||||||||||| || || || || |
SBJCT: 20   GACACCGCTCTTTGACGAGAGGCCGGTGCGGGAAGGAGTGTCGCTATACTAGTTCTTCAC 79

QUERY: 359  TGGACAGTGAGGACTGCCGGGTGCCCACACAGAAATCCTACAGCTCCAGTGAGACTCTGA 418
            | |||||||| |||||| | || ||  | ||||| |||||||||||||||||||| ||||
SBJCT: 80   TCGACAGTGAAGACTGCAGAGTACCAGCTCAGAAGTCCTACAGCTCCAGTGAGACCCTGA 139

QUERY: 419  AGGCCTATGACCATGACAGCAGGATGCACTATGGAAACCGAGTCACAGACCTCATCCACC 478
            | || |||| ||||||||  ||||||||||| ||||| |||||  |||||||  | |||
SBJCT: 140  AAGCATATGGCCATGACACGAGGATGCACTACGGAAATCGAGTTTCAGACCTGGTTCACA 199

QUERY: 479  GGGAGTCAGATGAGTTTCCTAGACAAGGAACCAACTTCACCCTTGCCGAACTGGGCATCT 538
            ||||||| ||||||||||| || |||||||| |||||||||||||| |||||||| ||||
SBJCT: 200  GGGAGTCGGATGAGTTTCCAAGGCAAGGAACGAACTTCACCCTTGCAGAACTGGGAATCT 259

QUERY: 539  GTGAGCCCTCCCCACACCGAAGCGGCTACTGCTCCGACATGGGGATCCTTCACCAGGGCT 598
            |||||||||| || || ||||| ||||||||||| ||||| || || || || || ||||
SBJCT: 260  GTGAGCCCTCTCCCCATCGAAGTGGCTACTGCTCGGACATAGGAATACTCCATCAAGGCT 319

QUERY: 599  ACTCCCTTAGCACAGGGTCTGACGCCGACTCCGACACCGAGGGAGGGATGTCTCCAGAAC 658
            | ||| | ||||| || ||||| || ||||| ||||| ||||| |||||||||||||| |
SBJCT: 320  ATTCCTTGAGCACTGGCTCTGATGCTGACTCAGACACGGAGGGCGGGATGTCTCCAGAGC 379

QUERY: 659  ACGCCATCAGACTGTGGGGCAGAGGGATAAAATCCAGGCGCAGTTCCGGCCTGTCCAGTC 718
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SBJCT: 380 ACGCGATCAGGCTGTGGGGAAGAGGGATCAAATCCAGCCGAAGTTCTGGCCTGTCAAGTC 439

QUERY: 719 GTGAAAACTCGGCCCTTACCCTGACTGACTCTGACAACGAAAACAAATCAGATGA 773
           |||||||||||| || || || |||||||| ||||| || ||||| ||||||||
SBJCT: 440 GTGAAAACTCGGCTCTCACGCTCACTGACTCCGACAATGAGAACAAGTCAGATGA 494
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The full FCTR3a amino acid sequence also has 342 of 383 amino acid residues (89%) identical to, and 342 of 383 residues (89%) positive with, the 276 amino acid residue Odd Oz/ten-m homolog 2 (*Drosophila*) (GenBank Acc: NP_035986.2) (SEQ ID NO:68) (Table 3P).

Table 3P. BLASTP of FCTR3a against Odd Oz/ten-m homolog 2 - (SEQ ID NO:68)

```
>GI|7657415|REF|NP_035986.2| ODD OZ/TEN-M HOMOLOG 2 (DROSOPHILA); ODD OZ/TEN-M HOMOLOG
3
          (DROSOPHILA) [MUS MUSCULUS]
 GI|4760778|DBJ|BAA77397.1| (AB025411) TEN-M2 [MUS MUSCULUS]
         LENGTH = 2764

 SCORE =  495 BITS (1274), EXPECT = E-139
 IDENTITIES = 342/383 (89%), POSITIVES = 342/383 (89%), GAPS = 41/383 (10%)

QUERY: 37  HNPPPVSCQMPLLDSNTSHQIMDTNPDEEFSPNSYLLRACSGPQQASSSGPPNHHSQSTL 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 189 HNPPPVSCQMPLLDSNTSHQIMDTNPDEEFSPNSYLLRACSGPQQASSSGPPNHHSQSTL 248

QUERY: 97  RPPLPPPHNHTLSHHHSSANSLNRNSLTNRRSQIHAPAPAPNDLATTPESVQLQDSWVLN 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 249 RPPLPPPHNHTLSHHHSSANSLNRNSLTNRRSQIHAPAPAPNDLATTPESVQLQDSWVLN 308

QUERY: 157 SNVPLETRHFLFKTSSGSTPLFSSSSPGYPLTSGTVYTPPPRLLPRNTFSRKAFKLKKPS 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 309 SNVPLETRHFLFKTSSGSTPLFSSSSPGYPLTSGTVYTPPPRLLPRNTFSRKAFKLKKPS 368

QUERY: 217 KYCSWKCAALSAIAAALLLAILLAYFI--------------------------------- 243
           |||||||||||||||||||||||||||
SBJCT: 369 KYCSWKCAALSAIAAALLLAILLAYFIAMHLLGLNWQLQPADGHTFNNGVRTGLPGNDDV 428

QUERY: 244 --------VPWSLKNSSIDSGEAEVGRRVTQEVPPGVFWRSQIHISQPQFLKFNISLGKD 295
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 429 ATVPSGGKVPWSLKNSSIDSGEAEVGRRVTQEVPPGVFWRSQIHISQPQFLKFNISLGKD 488

QUERY: 296 ALFGVYIRRGLPPSHAQYDFMERLDGKEKWSVVESPRERRSIQTLVQNEAVFVQYLDVGL 355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 489 ALFGVYIRRGLPPSHAQYDFMERLDGKEKWSVVESPRERRSIQTLVQNEAVFVQYLDVGL 548

QUERY: 356 WHLAFYNDGKDKEMVSFNTVVLD 378
           |||||||||||||||||||||||
SBJCT: 549 WHLAFYNDGKDKEMVSFNTVVLD 571
```

The full FCTR3b amino acid sequence has 2442 of 2802 amino acid residues (87%) identical to, and 2532 of 2802 residues (90%) positive with, the 2802 amino acid residue teneurin-2 [*Gallus gallus*] (GenBank Acc: AJ279031) (SEQ ID NO:69) (Table 3Q).

Table 3Q. BLASTP of FCTR3a against Teneurin-2 - (SEQ ID NO:69

```
>GI|10241574|EMB|CAC09416.1| (AJ279031) TENEURIN-2 [GALLUS GALLUS]
          LENGTH = 2802

 SCORE = 4853 BITS (12589), EXPECT = 0.0
 IDENTITIES = 2510/2802 (87%), POSITIVES = 2600/2802 (90%), GAPS = 69/2802 (2%)
```

```
QUERY: 1     MDVKDRRHRSLTRGRCGKECRYTSSSLDSEDCRVPTQKSYSSSETLKAYDHDSRMHYGNR 60
             ||+||||||||||||||||||||||||||||||| ||||||||||||||| ||+||||||
SBJCT: 1     MDIKDRRHRSLTRGRCGKECRYTSSSLDSEDCRVPAQKSYSSSETLKAYGHDTRMHYGNR 60

QUERY: 61    VTDLIHRESDEFPRQGTNFTLAELGICEPSPHRSGYCSDMGILHQGYSLSTGSDADSDTE 120
             |+||+|||||||||||||||||||||||||||||||||||+|||||||||||||||||||
SBJCT: 61    VSDLVHRESDEFPRQGTNFTLAELGICEPSPHRSGYCSDIGILHQGYSLSTGSDADSDTE 120

QUERY: 121   GGMSPEHAIRLWGRGIKSRRSSGLSSRENSALTLTDSDNENKSDDENG------------ 168
             |||||||||||||||||| ||||||||||||||||||||||||| ||
SBJCT: 121   GGMSPEHAIRLWGRGIKSSRSSGLSSRENSALTLTDSDNENKSDEENDFHTHLSEKLKDR 180

QUERY: 169   ----------------RPIPPTSSPSLLPSAQLPSSHNPPPVSCQMPLLDSNTSHQIMDT 212
                             |||||||| |||||||||||||||||||||||||||||||||||
SBJCT: 181   QTSWQQLAETKNSLIRRPIPPTSSSSLLPSAQLPSSHNPPPVSCQMPLLDSNTSHQIMDT 240

QUERY: 213   NPDEEFSPNSYLLRACSGPQQASSSGPPNHHSQSTLRPPLPPPHNHTLSHHHSSANSLNR 272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 241   NPDEEFSPNSYLLRACSGPQQASSSGPSNHHSQSTLRPPLPPPHNHSLSHHHSSANSLNR 300

QUERY: 273   XXXXXXXXQIHAPAPAPNDLATTPESVQLQDSWVLNSNVPLETRHFLFKXXXXXXXXXXX 332
                     |||||||||||||||||||||||||||||||||||||||||
SBJCT: 301   NSLTNRRNQIHAPAPAPNDLATTPESVQLQDSWVLNSNVPLETRHFLFKTSSGTTPLFSS 360

QUERY: 333   XXXXYPLTSGTVYTPPPRLLPRNTFSRKAFKLKKPSKYCSWKCXXXXXXXXXXXXXXXXX 392
                 ||||||||||||||||||||||| |||||||||||||||
SBJCT: 361   SSPGYPLTSGTVYTPPPRLLPRNTFSRNAFKLKKPSKYCSWKCAALSAIAAAVLLAILLA 420

QUERY: 393   YFIV-----------------------------------------PWSLKNSSIDSGEAE 411
             |||                                          ||  +||||||||| |
SBJCT: 421   YFIAMHLLGLNWQLQPADGHTFSNGLRPGAAGAEDGAAAPPAGRGPWVTRNSSIDSGETE 480

QUERY: 412   VGRRVTQEVPPGVFWRSQIHISQPQFLKFNISLGKDALFGVYIRRGLPPSHAQYDFMERL 471
             |||+||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 481   VGRKVTQEVPPGVFWRSQIHISQPQFLKFNISLGKDALFGVYIRRGLPPSHAQYDFMERL 540

QUERY: 472   DGKEKWSVVESPRERRSIQTLVQNEAVFVQYLDVGLWHLAFYNDGKDKEMVSFNTVVLDS 531
             |||||||||||||||||||||||||||||||||||||||||||||||||+|||+||+|||
SBJCT: 541   DGKEKWSVVESPRERRSIQTLVQNEAVFVQYLDVGLWHLAFYNDGKDKEVVSFSTVILDS 600

QUERY: 532   VQDCPRNCHGNGECVSGVCHCFPGFLGADCAKAACPVLCSGNGQYSKGTCQCYSGWKGAE 591
             ||||||||||||||||||||||||| |||||||||||||||||||||||| ||||||| |
SBJCT: 601   VQDCPRNCHGNGECVSGVCHCFPGFHGADCAKAACPVLCSGNGQYSKGTCLCYSGWKGPE 660

QUERY: 592   CDVPMNQCIDPSCGGHGSCIDGNCVCSAGYKGEHCEEVDCLDPTCSSHGVCVNGECLCSP 651
             ||||++||||||||||||||+|||||| |||||+||||||||||||+|||||||||||||
SBJCT: 661   CDVPISQCIDPSCGGHGSCIEGNCVCSIGYKGENCEEVDCLDPTCSNHGVCVNGECLCSP 720

QUERY: 652   GWGGLNCELARVQCPDQCSGHGTYLPDTGLCSCDPNWMGPDCSVEVCSVDCGTHGVCIGG 711
             ||||+|||| | ||||||||||||| ||||||||||||||||||||||||||||||||||
SBJCT: 721   GWGGINCELPRAQCPDQCSGHGTYLSDTGLCSCDPNWMGPDCSVEVCSVDCGTHGVCIGG 780

QUERY: 712   ACRCEEGWTGAACDQRVCHPRCIEHGTCKDGKCECREGWNGEHCTIGRQTAGTETDGCPD 771
             |||||||||| ||||||||||| ||||||||||||||||||||||||||| |||||||||
SBJCT: 781   ACRCEEGWTGVACDQRVCHPRCTEHGTCKDGKCECREGWNGEHCTIGRQTTGTETDGCPD 840

QUERY: 772   LCNGNGRCTLGQNSWQCVCQTGWRGPGCNVAMETSCADNKDNEGDGLVDCLDPDCCLQSA 831
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
SBJCT: 841   LCNGNGRCTLGQNSWQCVCQTGWRGPGCNVAMETSCADNKDNEGDGLVDCLVPDCCLQST 900

QUERY: 832   CQNSLLCRGSRDPLDIIQQGQTDWPAVKSFYDRIKLLAGKDSTHIIPGENPFNSSLVSLI 891
             |||||||||||||||||||  +  ||||||||||||| ||||||||||||||||||||||
SBJCT: 901   CQNSLLCRGSRDPLDIIQQSHSGSPAVKSFYDRIKLLVGKDSTHIIPGENPFNSSLVSLI 960

QUERY: 892   RGQVVTTDGTPLVGVNVSFVKYPKYGYTITRQDGTFDLIANGGASLTLHFERAPFMSQER 951
             |||||||||||||||||||||||||||||||||| |||+||||+||||||||||||||||
SBJCT: 961   RGQVVTTDGTPLVGVNVSFVKYPKYGYTITRQDGMFDLVANGGSSLTLHFERAPFMSQER 1020

QUERY: 952   TVWLPWNSFYAMDTLVMKTEENSIPSCDLSGFVRPDPIIISSPLSTFFSAAPGQNPIVPE 1011
             |||||||||||||||||||||||||||||||||||||+||||||||||| |||+||||||
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```
SBJCT: 1021 TVWLPWNSFYAMDTLVMKTEENSIPSCDLSGFVRPDPVIISSPLSTFFSDAPGRNPIVPE 1080

QUERY: 1012 TQVLHEEIELPGSNVKLRYLSSRTAGYKSLLKITMTQSTVPLNLIRVHLMVAVEGHLFQK 1071
            |||||||||+|||++|| ||||||||||||||| |||| ||||||+||||||||||||||
SBJCT: 1081 TQVLHEEIEVPGSSIKLIYLSSRTAGYKSLLKIIMTQSLVPLNLIKVHLMVAVEGHLFQK 1140

QUERY: 1072 SFQASPNLASTFIWDKTDAYGQRVYGLSDAVVSVGFEYETCPSLILWEKRTALLQGFELD 1131
            || |||||| ||||||||||||+|||||||||||||||||||||||||||||||||||||
SBJCT: 1141 SFLASPNLAYTFIWDKTDAYGQKVYGLSDAVVSVGFEYETCPSLILWEKRTALLQGFELD 1200

QUERY: 1132 PSNLGGWSLDKHHILNVKSGILHKGTGENQFLTQQPAIITSIMGNGRRRSISCPSCNGLA 1191
            |||||||||||||+||||||||||| |||||||||||+||||||||||||||||||||||
SBJCT: 1201 PSNLGGWSLDKHHVLNVKSGILHKGNGENQFLTQQPAVITSIMGNGRRRSISCPSCNGLA 1260

QUERY: 1192 EGNKLLAPVALAVGIDGSLYVGDFNYIRRIFPSRNVTSILELRNKEFKHSNNPAHKYYLA 1251
            |||||||||||||||||||+||||||||||||||||||||||||||||||||||||||||
SBJCT: 1261 EGNKLLAPVALAVGIDGSLFVGDFNYIRRIFPSRNVTSILELRNKEFKHSNNPAHKYYLA 1320

QUERY: 1252 VDPVSGSLYVSDTNSRRIYRVKSLSGTKDLAGNSEVVAGTGEQCLPFDEARCGDGGKAID 1311
            |||||||||||||||||||+||||+||||||||||||||||||||||||||||||||||+|
SBJCT: 1321 VDPVSGSLYVSDTNSRRIYKVKSLTGTKDLAGNSEVVAGTGEQCLPFDEARCGDGGKAVD 1380

QUERY: 1312 ATLMSPRGIAVDKNGLMYFVDATMIRKVDQNGIISTLLGSNDLTAVRPLSCDSSMDVAQV 1371
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||+||
SBJCT: 1381 ATLMSPRGIAVDKYGLMYFVDATMIRKVDQNGIISTLLGSNDLTAVRPLSCDSSMDVSQV 1440

QUERY: 1372 RLEWPTDLAVNPMDNSLYVLENNVILRITENHQVSIIAGRPMHCQVPGIDYSLSKXXXXXX 1431
            ||||||||||+|||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1441 RLEWPTDLAVDPMDNSLYVLENNVILRITENHQVSIIAGRPMHCQVPGIDYSLSKLAIHS 1500

QUERY: 1432 XXXXXXXXXXXXTGVLYITETDEKKINRLRQVTTNGEICLLAGAASXXXXXXXXXXXXYS 1491
                        ||||||+|||||||||||||||||||||||||||            ||
SBJCT: 1501 ALESASAIAISHTGVLYISETDEKKINRLRQVTTNGEICLLAGAASDCDCKNDVNCNCYS 1560

QUERY: 1492 GDDAYATDAILNSPSSLAVAPDGTIYIADLGNIRIRAVSKNKPVLNAFNQYEAASPGEQE 1551
            ||| |||||||||||||||||||||||||||||||||||||+|+||+|||||||||||||
SBJCT: 1561 GDDGYATDAILNSPSSLAVAPDGTIYIADLGNIRIRAVSKNRPILNSFNQYEAASPGEQE 1620

QUERY: 1552 LYVFNADGIHQYTVSLVTGEYLYNFTYSTDNDVTELIDNNGNSLKIRRDSSGMPRHLLMP 1611
            |||||||||||||+||||||||||||||+||||||++|+||||||+|||+||||||||||
SBJCT: 1621 LYVFNADGIHQYTLSLVTGEYLYNFTYSSDNDVTEVMDSNGNSLKVRRDASGMPRHLLMP 1680

QUERY: 1612 DNQIITLTVGTNGGLKVVSTQNLELGLMTYDGNTGLLATKSDETGWTTFYDYDHEGRLTN 1671
            ||||+|| ||||||||+|||| ||||||||+||+||||||||||||||||||||||||||
SBJCT: 1681 DNQIVTLAVGTNGGLKLVSTQTLELGLMTYNGNSGLLATKSDETGWTTFYDYDHEGRLTN 1740

QUERY: 1672 VTRPTGVVTSLHREMEKSITIDIENSNRDDDVTVITNLSSVEASYTVVQDQVRNSYQLCN 1731
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1741 VTRPTGVVTSLHREMEKSITIDIENSNRDDDVTVITNLSSVEASYTVVQDQVRNSYQLCN 1800

QUERY: 1732 NGTLRVMYANGMGISFHSEPHVLAGTITPTIGRCNISLPMENGLNSIEWRLRKEQIKGKV 1791
            |||||||||||| |||||||||||||+|||||||||||||||||||||||||||||||||
SBJCT: 1801 NGTLRVMYANGMSISFHSEPHVLAGTVTPTIGRCNISLPMENGLNSIEWRLRKEQIKGKV 1860

QUERY: 1792 TIFGRKLRVHGRNLLSIDYDRNIRTEKIYDDHRKFTLRIIYDQVGRPFLWLPSSGLAAVN 1851
            |+|||||||||||||||||||||||||||||||||||||||||+||||||||||||||||
SBJCT: 1861 TVFGRKLRVHGRNLLSIDYDRNIRTEKIYDDHRKFTLRIIYDQLGRPFLWLPSSGLAAVN 1920

QUERY: 1852 VSYFFNGRLAGLQRGAMSERTDIDKQGRIVSRMFADGKVWSYSYLDKSMVLLLQSQRQYI 1911
            |||||||||||||||||||||||||||||+||||||||||||+||+||||||||||||||
SBJCT: 1921 VSYFFNGRLAGLQRGAMSERTDIDKQGRIISRMFADGKVWSYTYLEKSMVLLLQSQRQYI 1980

QUERY: 1912 FEYDSSDRLLAVTMPSVARHSMSTHTSIGYIRNIYNPPESNASVIFDYSDDGRILKTSFL 1971
            ||||||||| |||||||||||||||||+||||||||||||||||||||||||||||||||
SBJCT: 1981 FEYDSSDRLHAVTMPSVARHSMSTHTSVGYIRNIYNPPESNASVIFDYSDDGRILKTSFL 2040

QUERY: 1972 GTGRQVFYKYGKLSKLSEIVYDSTAVTFGYDETTGVLKMVNLQSGGFSCTIRYRKIGPLV 2031
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2041 GTGRQVFYKYGKLSKLSEIVYDSTAVTFGYDETTGVLKMVNLQSGGFSCTIRYRKIGPLV 2100
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```
QUERY: 2032 DKQIYRFSEEGMVNARFDYTYHDNSFRIASIKPVISETPLPVDLYRYDEISGKVEHFGKF 2091
            |||||||||||||||||||||||||||||||||+||||||||||||||||||||||||||
SBJCT: 2101 DKQIYRFSEEGMVNARFDYTYHDNSFRIASIKPIISETPLPVDLYRYDEISGKVEHFGKF 2160

QUERY: 2092 GVIYYDINQIITTAVMTLSKHFDTHGRIKEVQYEMFRSLMYWMTVQYDSMGRVIKRELKL 2151
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
SBJCT: 2161 GVIYYDINQIITTAVMTLSKHFDTHGRIKEVQYEMFRSLMYWMTVQYDSMGRVTKRELKL 2220

QUERY: 2152 GPYANTTKYTYDYDGDGQLQSVAVNDRPTWRYSYDXXXXXXXXXXXXSVRLMPLRYDLRD 2211
            |||||||||||||||||||||||||||||||||||            |||||||||||||
SBJCT: 2221 GPYANTTKYTYDYDGDGQLQSVAVNDRPTWRYSYDLNGNLHLLNPGNSVRLMPLRYDLRD 2280

QUERY: 2212 RITRLGDVQYKIDDDGYLCQRGSDIFEYNSKGLLTRAYNKASGWSVQYRYDGVGRRASYK 2271
            |||||||+ |||||||+|||||||+||||||||||||||||+||+|||||||+||||| |
SBJCT: 2281 RITRLGDIPYKIDDDGFLCQRGSDVFEYNSKGLLTRAYNKANGWNVQYRYDGLGRRASCK 2340

QUERY: 2272 TNLGHHLQYFYSDLHNPTRITHVYNHSNSEITSLYYDLQGHLFAMESSSGEEYYVASDNT 2331
            |||||||||||+|||||||+||||||||||||||||||||||||||||||||||||||||
SBJCT: 2341 TNLGHHLQYFYADLHNPTRVTHVYNHSNSEITSLYYDLQGHLFAMESSSGEEYYVASDNT 2400

QUERY: 2332 GTPLAVFSINGLMIKQLQYTAYGEIYYDSNPDFQMVIGFHGGLYDPLTKLVHFTQRDYDV 2391
            ||||||||||||||||||||||||||||||||||+|||||||||||||||||||||||||
SBJCT: 2401 GTPLAVFSINGLMIKQLQYTAYGEIYYDSNPDFQLVIGFHGGLYDPLTKLVHFTQRDYDV 2460

QUERY: 2392 LAGRWTSPDYTMWKNVGKEPAPFNLYMFKSNNPLSSELDLKNYVTDVKSWLVMFGFQLSN 2451
            |||||||||||||||+|+|||||||||||||||||+||||||||||||||||||||||||
SBJCT: 2461 LAGRWTSPDYTMWKNIGREPAPFNLYMFKSNNPLSNELDLKNYVTDVKSWLVMFGFQLSN 2520

QUERY: 2452 IIPGFPRAKMYFVPPPYELSESQASENGQLITGVQQTTERHNQAFMALEGQVITKKLHAS 2511
            ||||||||||||| |||||+|||| ||||||||||||||||||||||||||||+|+||||
SBJCT: 2521 IIPGFPRAKMYFVSPPYELTESQACENGQLITGVQQTTERHNQAFMALEGQVISKRLHAS 2580

QUERY: 2512 IREKAGHWFATTTPIIGKGIMFAIKEGRVTTGVSSIASEDSRKVASVLNNAYYLDKMHYS 2571
            |||||||||||+|||||||||||+|+||||||+||||++||||+|||||+|+||+|||||
SBJCT: 2581 IREKAGHWFATSTPIIGKGIMFAVKKGRVTTGISSIATDDSRKIASVLNSAHYLEKMHYS 2640

QUERY: 2572 IEGKDTHYFVKIGSADGDLVTLGTTIGRKVLESGVNVTVSQPTLLVNGRTRRFTNIEFQY 2631
            |||||||||||||||| |||||  | |||||+|||||||||||||+||||||||||||||
SBJCT: 2641 IEGKDTHYFVKIGSADSDLVTLAMTSGRKVLDSGVNVTVSQPTLLINGRTRRFTNIEFQY 2700

QUERY: 2632 STLLLSIRYGLTPDTLDEEKARVLDQARQRALGTAWAKEQQKARDGREGSRLWTEGEKQQ 2691
            ||||++|||||| ||||||||||||||||||||+|||||||||||||||||+||+|||||
SBJCT: 2701 STLLINIRYGLTADTLDEEKARVLDQARQRALGSAWAKEQQKARDGREGSRVWTDGEKQQ 2760

QUERY: 2692 LLSTGRVQGYEGYYVLPVEQYPELADSSSNIQFLRQNEMGKR 2733
            ||+|||||||||||||||||||||||||||||||||||||||
SBJCT: 2761 LLNTGRVQGYEGYYVLPVEQYPELADSSSNIQFLRQNEMGKR 2802
```

The FCTR3bcde and f amino acid sequences have 1524 of 2352 amino acid residues (64%) identical to, and 1881 of 2532 residues (79%) positive with, the amino acid residues 429-2771, 93 of 157 residues (59%) identical to and 118 of 157 residues (74%) positive with amino acid residues 1-155, and 59 of 152 residues (38%) identical to and 68 of 152 residues (43%) positive with amino acid residues 211-361 of Ten-m4 [*Mus musculus*] (ptnr: GenBank Acc: BAA77399.1) (SEQ ID NO:70) (Table 3R).

Table 3R. BLASTP of FCTR3b, c, d, e, and f against *Mus musculus* Ten-m4 - (SEQ ID NO:70)

```
>GI|4760782|DBJ|BAA77399.1| (AB025413) TEN-M4 [MUS MUSCULUS]
          LENGTH = 2771

 SCORE = 3089 BITS (8008), EXPECT = 0.0
```

```
IDENTITIES = 1524/2352 (64%), POSITIVES = 1881/2352 (79%), GAPS = 28/2352 (1%)

QUERY: 401  KNSSIDSGEAEVGRRVTQEVPPGVFWRSQIHISQPQFLKFNISLGKDALFGVYIRRGLPP 460
            ++| |||||  +||||  +|++|||  |||||+ |   |   ||||+||||  ||  |+| |+||||
SBJCT: 429  EDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLKFNVSLGKAALVGIYGRKGLPP 488

QUERY: 461  SHAQYDFMERLDGK-----EKWSVVESPRERRSIQTLVQNEAVFVQYLDVGLWHLAFYND 515
            || |+||+| |||+       |   |+     |+ |         +|  |+||||  |+|||||||
SBJCT: 489  SHTQFDFVELLDGRRLLTQEARSLEGPQRQSRGPVPPSSHETGFIQYLDSGIWHLAFYND 548

QUERY: 516  GKDKEMVSFNTVVLDSVQDCPRNCHGNGECVSGVCHCFPGFLGADCAKAACPVLCSGNGQ 575
            ||+ |+|||  |   ++||  +||  ||+|||+|+||  ||||  ||||  ||  +|+|||||||||
SBJCT: 549  GKESEVVSFLTTAIESVDNCPSNCYGNGDCISGTCHCFLGFLGPDCGRASCPVLCSGNGQ 608

QUERY: 576  YSKGTCQCYSGWKGAECDVPMNQCIDPSCGGHGSCIDGNCVCSAGYKGEHCEEVDCLDPT 635
            |  ||  |  |+|||||||||||  |||||  +|   ||+||  |  |+|+  |||||  ||||||+|||
SBJCT: 609  YMKGRCLCHSGWKGAECDVPTNQCIDVACSSHGTCIMGTCICNPGYKGESCEEVDCMDPT 668

QUERY: 636  CSSHGVCVNGECLCSPGWGGLNCELARVQCPDQCSGHGTYLPDTGLCSCDPNWMGPDCSV 695
            |||  ||||  |||  ||  ||||  |||    |    |  ||||||||+|||||||+|||+|  |  |||+
SBJCT: 669  CSSRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTFLPDTGLCNCDPSWTGHDCSI 728

QUERY: 696  EVCSVDCGTHGVCIGGACRCEEGWTGAACDQRVCHPRCIEHGTCKDGKCECREGWNGEHC 755
            |+|+  |||  ||||+||  ||||+||  |||||||  |||||  |||||+||||||    |||||||
SBJCT: 729  EICAADCGGHGVCVGGTCRCEDGWMGAACDQRACHPRCAEHGTCRDGKCECSPGWNGEHC 788
              *********
QUERY: 756  TIGRQTAGTETDGCPDLCNGNGRCTLGQNSWQCVCQTGWRGPGCNVAMETSCADNKDNEG 815
            ||          +|||  ||||||||||   |  |  ||||  ||||  ||+  +|||  |  |  |||+|
SBJCT: 789  TIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHCVCQLGWRGTGCDTSMETGCGDGKDNDG 848

QUERY: 816  DGLVDCLDPDCCLQSACQNSLLCRGSRDPLDIIQQGQT--DWPAVKSFYDRIKLLAGKDS 873
            ||||||+|||||||    |    +  ||  ||  |||||||+  |           +   ||||||  |  |+||
SBJCT: 849  DGLVDCMDPDCCLQPLCHVNPLCLGSPDPLDIIQETQAPVSQQNLNPFYDRIKFLVGRDS 908

QUERY: 874  THIIPGENPFNSSLVSLIRGQVVTTDGTPLVGVNVSFVKYPKYGYTITRQDGTFDLIANG 933
            ||  |||||||+         +|||||+|+|||||||||+||+   |  +||||+||||+|||+  ||
SBJCT: 909  THSIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFINNPLFGYTISRQDGSFDLVTNG 968

QUERY: 934  GASLTLHFERAPFMSQERTVWLPWNSFYAMDTLVMKTEENSIPSCDLSGFVRPDPIIISS 993
            |  |+  |  ||||||++||  |+||||+  |+  |+|+||+  |||  |||||||  |  ||+||++   |
SBJCT: 969  GISIILRFERAPFITQEHTLWLPWDRFFVMETIVMRHEENEIPSCDLSNFARPNPVVSPS 1028

QUERY: 994  PLSTFFSAAPGQNPIVPETQVLHEEIELPGSNVKLRYLSSRTAGYKSLLKITMTQSTVPL 1053
            ||++|  |+    +  |||||  |  |  |||  +  |    ++|  ||||||  ||||+|+|++|   |+|
SBJCT: 1029 PLTSFASSCAEKGPIVPEIQALQEEIVIAGCKMRLSYLSSRTPGYKSVLRISLTHPTIPF 1088

QUERY: 1054 NLIRVHLMVAVEGHLFQKSFQASPNLASTFIWDKTDAYGQRVYGLSDAVVSVGFEYETCP 1113
            ||++||||||||||  ||+|  |  |+|+|+   |||||||  |  |+|+|  |+|  ||||+|||+||
SBJCT: 1089 NLMKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGFSEAFVSVGYEYESCP 1148

QUERY: 1114 SLILWEKRTALLQGFELDPSNLGGWSLDKHHILNVKSGILHKGTGENQFLTQQPAIITSI 1173
             ||||||||+|||+|+|  |  ||||||||||  ||++|||||||  |||||++|||  +|  ||
SBJCT: 1149 DLILWEKRTAVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGNGENQFVSQQPPVIGSI 1208

QUERY: 1174 MGNGRRRSISCPSCNGLAEGNKLLAPVALAVGIDGSLYVGDFNYIRRIFPSRNVTSILEL 1233
            ||||||||||||||||+||||||||||    |  |||||||||||||||||||  |||+|||+
SBJCT: 1209 MGNGRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFPSGNVTNILEM 1268

QUERY: 1234 RNKEFKHSNNPAHKYYLAVDPVSGSLYVSDTNSRRIYRVKSLSGTKDLAGNSEVVAGTGE 1293
            |||+|+||++||||||||  ||+||++++||||||+++|||  +    |||    |||||||||+
SBJCT: 1269 RNKDFRHSHSPAHKYYLATDPMSGAVFLSDTNSRRVFKVKSTTVVKDLVKNSEVVAGTGD 1328

QUERY: 1294 QCLPFDEARCGDGGKAIDATLMSPRGIAVDKNGLMYFVDATMIRKVDQNGIISTLLGSND 1353
            ||||||+  ||||||||  +|||  +||||  |||  ||+||||  ||||+||||||||||||||
SBJCT: 1329 QCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRVDQNGIISTLLGSND 1388

QUERY: 1354 LTAVRPLSCDSSMDVAQQVRLEWPTDLAVNPMDNSLYVLENNVILRITENHQVSIIAGRPM 1413
            ||+  |||||||  |+++|||||||||||+||||||||||+|||+|+|+|||||  |+|||||
SBJCT: 1389 LTSARPLSCDSVMEISQVRLEWPTDLAINPMDNSLYVLDNNVVLQISENHQVRIVAGRPM 1448
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QUERY: 1414 HCQVPGID-YSLSKXXXXXXXXXXXXXXXXXTGVLYITETDEKKINRLRQVTTNGEICLL 1472
            |||||||| + |||                 ||||| |||||||||+|||||+||| |+
SBJCT: 1449 HCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTSGEISLV 1508

QUERY: 1473 AGAASXXXXXXXXXXXXXYSGDDAYATDAILNSPSSLAVAPDGTIYIADLGNIRIRAVSKN 1532
            ||| |             +|||| || || ||+||||||  || +|+||||||||| + ||
SBJCT: 1509 AGAPSGCDCKNDANCDCFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRIRFIRKN 1568

QUERY: 1533 KPVLNAFNQYEAASPGEQELYVFNADGIHQYTVSLVTGEYLYNFTYSTDNDVTELIDNNG 1592
            || ||  | || +|| +||||+|+  | | || || ||+|||||||+ | |+| + ||||
SBJCT: 1569 KPFLNTQNMYELSSPIDQELYLFDTSGKHLYTQSLPTGDYLYNFTYTGDGDITHITDNNG 1628

QUERY: 1593 NSLKIRRDSSGMPRHLLMPDNQIITLTVGTNGGLKVVSTQNLELGLMTYDGNTGLLATKS 1652
            | + +||||+|||  |++|| |+  +|+|||  |+ |+||  || +||| ||+|||||||
SBJCT: 1629 NMVNVRRDSTGMPLWLVVPDGQVYWVTMGTNSALRSVTTQGHELAMMTYHGNSGLLATKS 1688

QUERY: 1653 DETGWTTFYDYDHEGRLTNVTRPTGVVTSLHREMEKSITIDIENSNRDDDVTVITNLSSV 1712
            +| ||||||+||  ||||||| ||| |+|  + + |+ + +| |++ ||||+ ||||+
SBJCT: 1689 NENGWTTFYEYDSFGRLTNVTFPTGQVSSFRSDTDSSVHVQVETSSK-DDVTITTNLSAS 1747

QUERY: 1713 EASYTVVQDQVRNSYQLCNNGTLRVMYANGMGISFHSEPHVLAGTITPTIGRCNISLPME 1772
             | ||++|||||||| +  +|+||++ ||||  ++  +|||+||||+ ||+|+ |++||++
SBJCT: 1748 GAFYTLLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRNVTLPID 1807

QUERY: 1773 NGLNSIEWRLRKEQIKGKVTIFGRKLRVHGRNLLSIDYDRNIRTEKIYDDHRKFTLRIIY 1832
            |||| +||| |||| +|+||+|||+|||| |||||+|+||  ||||||||||||||||+|
SBJCT: 1808 NGLNLVEWRQRKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFTLRILY 1867

QUERY: 1833 DQVGRPFLWLPSSGLAAVNVSYFFNGRLAGLQRGAMSERTDIDKQGRIVSRMFADGKVWS 1892
            || ||| || ||| |  |||+|   | +||+|||  |||| + |+ ||| ||+|||||+||
SBJCT: 1868 DQAGRPSLWSPSSRLNGVNVTYSPGGHIAGIQRGIMSERMEYDQAGRITSRIFADGKMWS 1927

QUERY: 1893 YSYLDKSMVLLLQSQRQYIFEYDSSDRLLAVTMPSVARHSMSTHTSIGYIRNIYNPPESN 1952
            |+||+|||||| | ||||||||+| +||| +||||+|||++   |  |+|| |||| ||| |
SBJCT: 1928 YTYLEKSMVLHLHSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYYRNIYQPPEGN 1987

QUERY: 1953 ASVIFDYSDDGRILKTSFLGTGRQVFYKYGKLSKLSEIVYDSTAVTFGYDETTGVLKMVN 2012
            |||| |+++||  +| | +|||||+| |||||||||+| +||+| |+| |||| |+|| ||
SBJCT: 1988 ASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGMLKTVN 2047

QUERY: 2013 LQSGGFSCTIRYRKIGPLVDKQIYRFSEEGMVNARFDYTYHDNSFRIASIKPVISETPLP 2072
            ||+ ||+||||||+||||+|+||+||+||||||||||| | |||||+ |++ ||+|||||
SBJCT: 2048 LQNEGFTCTIRYRQIGPLIDRQIFRFTEEGMVNARFDYNY-DNSFRVTSMQAVINETPLP 2106

QUERY: 2073 VDLYRYDEISGKVEHFGKFGVIYYDINQIITTAVMTLSKHFDTHGRIKEVQYEMFRSLMY 2132
            +||||||++||| | ||||||||||||||||||||| +|||| +||+||||||+||||||
SBJCT: 2107 IDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIFRSLMY 2166

QUERY: 2133 WMTVQYDSMGRVIKRELKLGPYANTTKYTYDYDGDGQLQSVAVNDRPTWRYSYDXXXXXX 2192
            |||||||+||||+|+|||+|||||||+|+|+|| |||||+|++||+| ||||||
SBJCT: 2167 WMTVQYDNMGRVVKKELKVGPYANTTRYSYEYDADGQLQTVSINDKPLWRYSYDLNGNLH 2226

QUERY: 2193 XXXXXXSVRLMPLRYDLRDRITRLGDVQYKIDDDGYLCQRGSDIFEYNSKGLLTRAYNKA 2252
                  | || |||||||||||||||||||+|+||+| ||| |+||||| ||| +|||+|
SBJCT: 2227 LLSPGNSARLTPLRYDLRDRITRLGDVQYKMDEDGFLRQRGGDVFEYNSAGLLIKAYNRA 2286

QUERY: 2253 SGWSVQYRYDGVGRRASYKTNLGHHLQYFYSDLHNPTRITHVYNHSNSEITSLYYDLQGH 2312
            |||||+|||||+||| | |++  ||||+||+|| |||++||+||||+|||||||||||||
SBJCT: 2287 SGWSVRYRYDGLGRRVSSKSSHSHHLQFFYADLTNPTKVTHLYNHSSSEITSLYYDLQGH 2346

QUERY: 2313 LFAMESSSGEEYYVASDNTGTPLAVFSINGLMIKQLQYTAYGEIYYDSNPDFQMVIGFHG 2372
            ||||| |||+|+|+| || ||||||||  ||||||+ |||||||| |+||+||++||+||
SBJCT: 2347 LFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIIIGYHG 2406

QUERY: 2373 GLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWKNVGKEP-APFNLYMFKSNNPLSSELDL 2431
            |||||||||||  +||||||||||||||+ +|| +      ||+|||||+|||+|+  |+
SBJCT: 2407 GLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKRLSSNSIVPFHLYMFKNNNPISNSQDI 2466

QUERY: 2432 KNYVTDVKSWLVMFGFQLSNIIPGFPRAKMYFVPPPYELSESQAS----ENGQLITGVQQ 2487
            | ++||| |||+ ||||| |+|||+|+      + | |||  +|      +| + | |||
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SBJCT: 2467 KCFMTDVNSWLLTFGFQLHNVIPGYPKPDTDAMEPSYELVHTQMKTQEWDNSKSILGVQC 2526

QUERY: 2488 TTERHNQAFMALE------GQVITKKLHASIREKAGHWFATTTPIIGKGIMFAIKEGRVT 2541
              ++   +||+ ||          |  ||      |     +|      ||++   |  |||+ ||+|+||||
SBJCT: 2527 EVQKQLKAFVTLERFDQLYGSTITSCQQAPETKK----FASSGSIFGKGVKFALKDGRVT 2582

QUERY: 2542 TGVSSIASEDSRKVASVLNNAYYLDKMHYSIEGKDTHYFVKIGSADGDLVTLGTTIGRKV 2601
            | +  |+|+||  |++|++||||+||+ +|++|+|  ||||||| | ++|||   || + ||+
SBJCT: 2583 TDIISVANEDGRRIAAILNNAHYLENLHFTIDGVDTHYFVKPGPSEGDLAILGLSGGRRT 2642

QUERY: 2602 LESGVNVTVSQPTLLVNGRTRRFTNIEFQYSTLLLSIRYGLTPDTLDEEKARVLDQARQR 2661
            ||+||||||||     +++|||||+|+|+ ||    |  |+ |||       |+|||| |||+ ||||
SBJCT: 2643 LENGVNVTVSQINTMLSGRTRRYTDIQLQYRALCLNTRYG---TTVDEEKVRVLELARQR 2699

QUERY: 2662 ALGTAWAKEQQKARDGREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADSSSN 2721
            |+   |||+|||+  |+|  ||  |  ||+|||||+|+|||||||+|++|   |||||||+||++|
SBJCT: 2700 AVRQAWAREQQRLREGEEGLRAWTDGEKQQVLNTGRVQGYDGFFVTSVEQYPELSDSANN 2759

QUERY: 2722 IQFLRQNEMGKR 2733
            |  |+||+|||+|
SBJCT: 2760 IHFMRQSEMGRR 2771

 SCORE =  161 BITS (407), EXPECT = 2E-37
 IDENTITIES = 93/157 (59%), POSITIVES = 118/157 (74%), GAPS = 4/157 (2%)

QUERY: 1    MDVKDRR-HRSLTRGRCGKECRYTSSSLDSEDCRVPTQKSYSSSETLKAYDHDSRMHYGN 59
            ||||+|+ +||||| |     | |||||| |||+ +  |  ||||||||||||| |+|+ ||+
SBJCT: 1    MDVKERKPYRSLTRRR-DAERRYTSSSADSEEGKGP-QKSYSSSETLKAYDQDARLAYGS 58

QUERY: 60   RVTDLIHRESDEFPRQGTNFTLAELGICEPS-PHRSGYCSDMGILHQGYSLSTGSDADSD 118
            || |++ +|++|| | |||||| |||+  |  +  ||  +  |  +|+|+ |  |||+     |||| +
SBJCT: 59   RVKDMVPQEAEEFCRTGTNFTLRELGLGEMTPPHGTLYRTDIGLPHCGYSMGASSDADLE 118

QUERY: 119  TEGGMSPEHAIRLWGRGIKSRRSSGLSSRENSALTLT 155
             +  +||||  +|||||   +|  |||  ||||  || ||||
SBJCT: 119  ADTVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLT 155

 SCORE = 72.1 BITS (176), EXPECT = 8E-11
 IDENTITIES = 59/152 (38%), POSITIVES = 68/152 (43%), GAPS = 42/152 (27%)

QUERY: 285  PAPAPND--LATTP------ESVQLQDSWVLNSNVPLETR-------------------- 316
            |+|||  |    |+    |            |       ||+|+||||+|||||
SBJCT: 211  PSPAPTDHSLSGEPPAGSAQEPTHAQDNWLLNSNIPLETRNLGKQPFLGTLQDNLIEMDI 270

QUERY: 317  -------------HFLFKXXXXXXXXXXXXXXXXYPLTSGTVYTPPPRLLPRNTFSRKAFK 363
                          |||||                 ||||| |||+|||| |||+|||| ||
SBJCT: 271  LSASRHDGAYSDGHFLFK-PGGTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTFSRPAFN 329

QUERY: 364  LKKPSKYCSWKCXXXXXXXXXXXXXXXXXXYFI 395
            ||||||||+|||                    ||+
SBJCT: 330  LKKPSKYCNWKCAALSAILISATLVILLAYFV 361

*FCTR3F DOES NOT CONTAIN THESE AMINO ACIDS
```

The 997-2733 amino acid fragment of the FCTR3bcde and f protein was also found to have 1695 of 1737 amino acid residues (97%) identical to, and 1695 of 1737 residues (97%) positive with the amino a 1737 amino acid residue protein KIAA1127 protein [*Homo sapiens*] (GenBank Acc:(AB032953) (SEQ ID NO:71), (Table 3S).

Table 3S. BLASTP of FCTR3b, c, d, e, and f against *Homo sapiens* KIAA1127 protein (SEQ ID NO:71)

```
>GI|6329763|DBJ|BAA86441.1| (AB032953) KIAA1127 PROTEIN [HOMO SAPIENS]
          LENGTH = 1737
```

```
SCORE = 3295 BITS (8545), EXPECT = 0.0
IDENTITIES = 1695/1737 (97%), POSITIVES = 1695/1737 (97%)

QUERY: 997  TFFSAAPGQNPIVPETQVLHEEIELPGSNVKLRYLSSRTAGYKSLLKITMTQSTVPLNLI 1056
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1    TFFSAAPGQNPIVPETQVLHEEIELPGSNVKLRYLSSRTAGYKSLLKITMTQSTVPLNLI 60

QUERY: 1057 RVHLMVAVEGHLFQKSFQASPNLASTFIWDKTDAYGQRVYGLSDAVVSVGFEYETCPSLI 1116
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
SBJCT: 61   RVHLMVAVEGHLFQKSFQASPNLAYTFIWDKTDAYGQRVYGLSDAVVSVGFEYETCPSLI 120

QUERY: 1117 LWEKRTALLQGFELDPSNLGGWSLDKHHILNVKSGILHKGTGENQFLTQQPAIITSIMGN 1176
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 121  LWEKRTALLQGFELDPSNLGGWSLDKHHILNVKSGILHKGTGENQFLTQQPAIITSIMGN 180

QUERY: 1177 GRRRSISCPSCNGLAEGNKLLAPVALAVGIDGSLYVGDFNYIRRIFPSRNVTSILELRNK 1236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 181  GRRRSISCPSCNGLAEGNKLLAPVALAVGIDGSLYVGDFNYIRRIFPSRNVTSILELRNK 240

QUERY: 1237 EFKHSNNPAHKYYLAVDPVSGSLYVSDTNSRRIYRVKSLSGTKDLAGNSEVVAGTGEQCL 1296
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 241  EFKHSNNPAHKYYLAVDPVSGSLYVSDTNSRRIYRVKSLSGTKDLAGNSEVVAGTGEQCL 300

QUERY: 1297 PFDEARCGDGGKAIDATLMSPRGIAVDKNGLMYFVDATMIRKVDQNGIISTLLGSNDLTA 1356
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 301  PFDEARCGDGGKAIDATLMSPRGIAVDKNGLMYFVDATMIRKVDQNGIISTLLGSNDLTA 360

QUERY: 1357 VRPLSCDSSMDVAQVRLEWPTDLAVNPMDNSLYVLENNVILRITENHQVSIIAGRPMHCQ 1416
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 361  VRPLSCDSSMDVAQVRLEWPTDLAVNPMDNSLYVLENNVILRITENHQVSIIAGRPMHCQ 420

QUERY: 1417 VPGIDYSLSKXXXXXXXXXXXXXXXXXTGVLYITETDEKKINRLRQVTTNGEICLLAGAA 1476
             ||||||||||                 |||||||||||||||||||||||||||||||||
SBJCT: 421  VPGIDYSLSKLAIHSALESASAIAISHTGVLYITETDEKKINRLRQVTTNGEICLLAGAA 480

QUERY: 1477 SXXXXXXXXXXXXYSGDDAYATDAILNSPSSLAVAPDGTIYIADLGNIRIRAVSKNKPVL 1536
             |            |||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 481  SDCDCKNDVNCNCYSGDDAYATDAILNSPSSLAVAPDGTIYIADLGNIRIRAVSKNKPVL 540

QUERY: 1537 NAFNQYEAASPGEQELYVFNADGIHQYTVSLVTGEYLYNFTYSTDNDVTELIDNNGNSLK 1596
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 541  NAFNQYEAASPGEQELYVFNADGIHQYTVSLVTGEYLYNFTYSTDNDVTELIDNNGNSLK 600

QUERY: 1597 IRRDSSGMPRHLLMPDNQIITLTVGTNGGLKVVSTQNLELGLMTYDGNTGLLATKSDETG 1656
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 601  IRRDSSGMPRHLLMPDNQIITLTVGTNGGLKVVSTQNLELGLMTYDGNTGLLATKSDETG 660

QUERY: 1657 WTTFYDYDHEGRLTNVTRPTGVVTSLHREMEKSITIDIENSNRDDDVTVITNLSSVEASY 1716
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 661  WTTFYDYDHEGRLTNVTRPTGVVTSLHREMEKSITIDIENSNRDDDVTVITNLSSVEASY 720

QUERY: 1717 TVVQDQVRNSYQLCNNGTLRVMYANGMGISFHSEPHVLAGTITPTIGRCNISLPMENGLN 1776
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 721  TVVQDQVRNSYQLCNNGTLRVMYANGMGISFHSEPHVLAGTITPTIGRCNISLPMENGLN 780

QUERY: 1777 SIEWRLRKEQIKGKVTIFGRKLRVHGRNLLSIDYDRNIRTEKIYDDHRKFTLRIIYDQVG 1836
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 781  SIEWRLRKEQIKGKVTIFGRKLRVHGRNLLSIDYDRNIRTEKIYDDHRKFTLRIIYDQVG 840

QUERY: 1837 RPFLWLPSSGLAAVNVSYFFNGRLAGLQRGAMSERTDIDKQGRIVSRMFADGKVWSYSYL 1896
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 841  RPFLWLPSSGLAAVNVSYFFNGRLAGLQRGAMSERTDIDKQGRIVSRMFADGKVWSYSYL 900

QUERY: 1897 DKSMVLLLQSQRQYIFEYDSSDRLLAVTMPSVARHSMSTHTSIGYIRNIYNPPESNASVI 1956
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 901  DKSMVLLLQSQRQYIFEYDSSDRLLAVTMPSVARHSMSTHTSIGYIRNIYNPPESNASVI 960

QUERY: 1957 FDYSDDGRILKTSFLGTGRQVFYKYGKLSKLSEIVYDSTAVTFGYDETTGVLKMVNLQSG 2016
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 961  FDYSDDGRILKTSFLGTGRQVFYKYGKLSKLSEIVYDSTAVTFGYDETTGVLKMVNLQSG 1020
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QUERY: 2017 GFSCTIRYRKIGPLVDKQIYRFSEEGMVNARFDYTYHDNSFRIASIKPVISETPLPVDLY 2076
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1021 GFSCTIRYRKIGPLVDKQIYRFSEEGMVNARFDYTYHDNSFRIASIKPVISETPLPVDLY 1080

QUERY: 2077 RYDEISGKVEHFGKFGVIYYDINQIITTAVMTLSKHFDTHGRIKEVQYEMFRSLMYWMTV 2136
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1081 RYDEISGKVEHFGKFGVIYYDINQIITTAVMTLSKHFDTHGRIKEVQYEMFRSLMYWMTV 1140

QUERY: 2137 QYDSMGRVIKRELKLGPYANTTKYTYDYDGDGQLQSVAVNDRPTWRYSYDXXXXXXXXXX 2196
            ||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1141 QYDSMGRVIKRELKLGPYANTTKYTYDYDGDGQLQSVAVNDRPTWRYSYDLNGNLHLLNP 1200

QUERY: 2197 XXSVRLMPLRYDLRDRITRLGDVQYKIDDDGYLCQRGSDIFEYNSKGLLTRAYNKASGWS 2256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1201 GNSVRLMPLRYDLRDRITRLGDVQYKIDDDGYLCQRGSDIFEYNSKGLLTRAYNKASGWS 1260

QUERY: 2257 VQYRYDGVGRRASYKTNLGHHLQYFYSDLHNPTRITHVYNHSNSEITSLYYDLQGHLFAM 2316
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1261 VQYRYDGVGRRASYKTNLGHHLQYFYSDLHNPTRITHVYNHSNSEITSLYYDLQGHLFAM 1320

QUERY: 2317 ESSSGEEYYVASDNTGTPLAVFSINGLMIKQLQYTAYGEIYYDSNPDFQMVIGFHGGLYD 2376
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1321 ESSSGEEYYVASDNTGTPLAVFSINGLMIKQLQYTAYGEIYYDSNPDFQMVIGFHGGLYD 1380

QUERY: 2377 PLTKLVHFTQRDYDVLAGRWTSPDYTMWKNVGKEPAPFNLYMFKSNNPLSSELDLKNYVT 2436
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1381 PLTKLVHFTQRDYDVLAGRWTSPDYTMWKNVGKEPAPFNLYMFKSNNPLSSELDLKNYVT 1440

QUERY: 2437 DVKSWLVMFGFQLSNIIPGFPRAKMYFVPPPYELSESQASENGQLITGVQQTTERHNQAF 2496
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1441 DVKSWLVMFGFQLSNIIPGFPRAKMYFVPPPYELSESQASENGQLITGVQQTTERHNQAF 1500

QUERY: 2497 MALEGQVITKKLHASIREKAGHWFATTTPIIGKGIMFAIKEGRVTTGVSSIASEDSRKVA 2556
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1501 MALEGQVITKKLHASIREKAGHWFATTTPIIGKGIMFAIKEGRVTTGVSSIASEDSRKVA 1560

QUERY: 2557 SVLNNAYYLDKMHYSIEGKDTHYFVKIGSADGDLVTLGTTIGRKVLESGVNVTVSQPTLL 2616
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1561 SVLNNAYYLDKMHYSIEGKDTHYFVKIGSADGDLVTLGTTIGRKVLESGVNVTVSQPTLL 1620

QUERY: 2617 VNGRTRRFTNIEFQYSTLLLSIRYGLTPDTLDEEKARVLDQARQRALGTAWAKEQQKARD 2676
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1621 VNGRTRRFTNIEFQYSTLLLSIRYGLTPDTLDEEKARVLDQARQRALGTAWAKEQQKARD 1680

QUERY: 2677 GREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADSSSNIQFLRQNEMGKR 2733
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1681 GREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADSSSNIQFLRQNEMGKR 1737
```

The amino acid sequences of the FCTR3bcde and f proteins were also found to have 2528 of 2774 amino acid residues (91%) identical to, and 2557 of 2774 residues (92%) positive with, the 2765 amino acid residue protein neurestin alpha [*Rattus norvegicus*] (GenBank Acc:AF086607) (SEQ ID NO:72), shown in Table 3T.

Table 3T. BLASTP of FCTR3bcd and f against *Rattus norvegicus* Neurestin alpha (SEQ ID NO:72)

```
>GI|9910320|REF|NP_064473.1| NEURESTIN ALPHA [RATTUS NORVEGICUS]
 GI|5712201|GB|AAD47383.1|AF086607_1 (AF086607) NEURESTIN ALPHA [RATTUS NORVEGICUS]
          LENGTH = 2765

 SCORE = 4988 BITS (12938), EXPECT = 0.0
 IDENTITIES = 2528/2774 (91%), POSITIVES = 2557/2774 (92%), GAPS = 50/2774 (1%)

QUERY: 1    MDVKDRRHRSLTRGRCGKECRYTSSSLDSEDCRVPTQKSYSSSETLKAYDHDSRMHYGNR 60
```

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1   MDVKDRRHRSLTRGRCGKECRYTSSSLDSEDCRVPTQKSYSSSETLKAYDHDSRMHYGNR 60

QUERY: 61  VTDLIHRESDEFPRQGTNFTLAELGICEPSPHRSGYCSDMGILHQGYSLSTGSDADSDTE 120
           ||||+||||||| ||| |||||||||||||||||||||||||||||||||||||||||||
SBJCT: 61  VTDLVHRESDEFSRQGANFTLAELGICEPSPHRSGYCSDMGILHQGYSLSTGSDADSDTE 120

QUERY: 121 GGMSPEHAIRLWGRGIKSRRSSGLSSRENSALTLTXXXXXXXXXXXXXGRXXXXXXXXXX 180
           |||||||||||||||||||||||||||||||||||             ||
SBJCT: 121 GGMSPEHAIRLWGRGIKSRRSSGLSSRENSALTLTDSDNENKSDDDNGRPIPPTSSSSLL 180

QUERY: 181 XXXXXXXXHNPPPVSCQMPLLDSNTSHQIMDTNPDEEFSPNSYLLRACXXXXXXXXXXXX 240
                   ||||||||||||||||||||||||||||||||||||||||
SBJCT: 181 PSAQLPSSHNPPPVSCQMPLLDSNTSHQIMDTNPDEEFSPNSYLLRACSGPQQASSSGPP 240

QUERY: 241 NHHSQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQIHAPAPAPNDLATTPESVQ 300
           |||||                                   ||||||||||||||||||||
SBJCT: 241 NHHSQSTLRPPLPPPHNHTLSHHHSSANSLNRNSLTNRRSQIHAPAPAPNDLATTPESVQ 300

QUERY: 301 LQDSWVLNSNVPLETRHFLFKXXXXXXXXXXXXXXYPLTSGTVVYTPPPRLLPRNTFSRK 360
           |||||||||||||||||||||              |||||||||||||||||||||||||
SBJCT: 301 LQDSWVLNSNVPLETRHFLFKTSSGSTPLFSSSSPGYPLTSGTVVYTPPPRLLPRNTFSRK 360

QUERY: 361 AFKLKKPSKYCSWKCXXXXXXXXXXXXXXXXXYFI------------------------- 395
           |||||||||||||||                 |||
SBJCT: 361 AFKLKKPSKYCSWKCAALSAIAAALLLAILLAYFIAMHLLGLNWQLQPADGHTFNNGVRT 420

QUERY: 396 ----------------VPWSLKNSSIDSGEAEVGRRVTQEVPPGVFWRSQIHISQPQFLK 439
                           ||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 421 GLPGNDDVATVPSGGKVPWSLKNSSIDSGEAEVGRRVTQEVPPGVFWRSQIHISQPQFLK 480

QUERY: 440 FNISLGKDALFGVYIRRGLPPSHAQYDFMERLDGKEKWSVVESPRERRSIQTLVQNEAVF 499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 481 FNISLGKDALFGVYIRRGLPPSHAQYDFMERLDGKEKWSVVESPRERRSIQTLVQNEAVF 540

QUERY: 500 VQYLDVGLWHLAFYNDGKDKEMVSFNTVVLDSVQDCPRNCHGNGECVSGVCHCFPGFLGA 559
           |||||||||||||||||||||||||||||||||||||||||||||||||+||||||||||
SBJCT: 541 VQYLDVGLWHLAFYNDGKDKEMVSFNTVVLDSVQDCPRNCHGNGECVSGLCHCFPGFLGA 600

QUERY: 560 DCAKAACPVLCSGNGQYSKGTCQCYSGWKGAECDVPMNQCIDPSCGGHGSCIDGNCVCSA 619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||+|
SBJCT: 601 DCAKAACPVLCSGNGQYSKGTCQCYSGWKGAECDVPMNQCIDPSCGGHGSCIDGNCVCAA 660

QUERY: 620 GYKGEHCEEVDCLDPTCSSHGVCVNGECLCSPGWGGLNCELARVQCPDQCSGHGTYLPDT 679
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||+
SBJCT: 661 GYKGEHCEEVDCLDPTCSSHGVCVNGECLCSPGWGGLNCELARVQCPDQCSGHGTYLPDS 720

QUERY: 680 GLCSCDPNWMGPDCSVEVCSVDCGTHGVCIGGACRCEEGWTGAACDQRVCHPRCIEHGTC 739
           |||+||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 721 GLCNCDPNWMGPDCSVEVCSVDCGTHGVCIGGACRCEEGWTGAACDQRVCHPRCIEHGTC 780
                             *********
QUERY: 740 KDGKCECREGWNGEHCTIGRQTAGTETDGCPDLCNGNGRCTLGQNSWQCVCQTGWRGPGC 799
           ||||||||||||||||||         |||||||||||||||||||||||||||||||||
SBJCT: 781 KDGKCECREGWNGEHCTI---------DGCPDLCNGNGRCTLGQNSWQCVCQTGWRGPGC 831

QUERY: 800 NVAMETSCADNKDNEGDGLVDCLDPDCCLQSACQNSLLCRGSRDPLDIIQQGQTDWPAVK 859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 832 NVAMETSCADNKDNEGDGLVDCLDPDCCLQSACQNSLLCRGSRDPLDIIQQGQTDWPAVK 891

QUERY: 860 SFYDRIKLLAGKDSTHIIPGENPFNSSLVSLIRGQVVTTDGTPLVGVNVSFVKYPKYGYT 919
           ||||||||||||||||||||+|||||||||||||||||||||||||||||||||||||||
SBJCT: 892 SFYDRIKLLAGKDSTHIIPGDNPFNSSLVSLIRGQVVTTDGTPLVGVNVSFVKYPKYGYT 951

QUERY: 920 ITRQDGTFDLIANGGASLTLHFERAPFMSQERTVWLPWNSFYAMDTLVMKTEENSIPSCD 979
           |||||||||||||||++||||||||||||+||||| ||||||||||||||||||||||||
SBJCT: 952 ITRQDGTFDLIANGGSALTLHFERAPFMSRERTVWPPWNSFYAMDTLVMKTEENSIPSCD 1011

QUERY: 980 LSGFVRPDPIIISSPLSTFFSAAPGQNPIVPETQVLHEEIELPGSNVKLRYLSSRTAGYK 1039
           ||||||||||||||||||||||+|  ||||||||||||||||||+|||||||||||||||
SBJCT: 1012 LSGFVRPDPIIISSPLSTFFSASPAANPIVPETQVLHEEIELPGTNVKLRYLSSRTAGYK 1071
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QUERY: 1040 SLLKITMTQSTVPLNLIRVHLMVAVEGHLFQKSFQASPNLASTFIWDKTDAYGQRVYGLS 1099
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
SBJCT: 1072 SLLKITMTQSTVPLNLIRVHLMVAVEGHLFQKSFQASPNLAYTFIWDKTDAYGQRVYGLS 1131

QUERY: 1100 DAVVSVGFEYETCPSLILWEKRTALLQGFELDPSNLGGWSLDKHHILNVKSGILHKGTGE 1159
            |||||||||||||||||||||||||||||||||||||||||||||  |||||||| |||||
SBJCT: 1132 DAVVSVGFEYETCPSLILWEKRTALLQGFELDPSNLGGWSLDKHHTLNVKSGILLKGTGE 1191

QUERY: 1160 NQFLTQQPAIITSIMGNGRRRSISCPSCNGLAEGNKLLAPVALAVGIDGSLYVGDFNYIR 1219
            |||||||||||||||||||||||||||||||||||||||||||||||||||+||||||||
SBJCT: 1192 NQFLTQQPAIITSIMGNGRRRSISCPSCNGLAEGNKLLAPVALAVGIDGSLFVGDFNYIR 1251

QUERY: 1220 RIFPSRNVTSILELRNKEFKHSNNPAHKYYLAVDPVSGSLYVSDTNSRRIYRVKSLSGTK 1279
            |||||||||||||||||||||||+| ||||||||||+||||||||||||||||||||| |
SBJCT: 1252 RIFPSRNVTSILELRNKEFKHSNSPGHKYYLAVDPVTGSLYVSDTNSRRIYRVKSLSGAK 1311

QUERY: 1280 DLAGNSEVVAGTGEQCLPFDEARCGDGGKAIDATLMSPRGIAVDKNGLMYFVDATMIRKV 1339
            ||||||||||||||||||||||||||||||+|||||||||||||||||||||||||||||
SBJCT: 1312 DLAGNSEVVAGTGEQCLPFDEARCGDGGKAVDATLMSPRGIAVDKNGLMYFVDATMIRKV 1371

QUERY: 1340 DQNGIISTLLGSNDLTAVRPLSCDSSMDVAQVRLEWPTDLAVNPMDNSLYVLENNVILRI 1399
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1372 DQNGIISTLLGSNDLTAVRPLSCDSSMDVAQVRLEWPTDLAVNPMDNSLYVLENNVILRI 1431

QUERY: 1400 TENHQVSIIAGRPMHCQVPGIDYSLSKXXXXXXXXXXXXXXXXXTGVLYITETDEKKINR 1459
            |||||||||||||||||||||||||||                 ||||||||||||||||
SBJCT: 1432 TENHQVSIIAGRPMHCQVPGIDYSLSKLAIHSALESASAIAISHTGVLYITETDEKKINR 1491

QUERY: 1460 LRQVTTNGEICLLAGAASXXXXXXXXXXXXYSGDDAYATDAILNSPSSLAVAPDGTIYIA 1519
            ||||||||||||||||||            ||||||||||||||||||||||||||||||
SBJCT: 1492 LRQVTTNGEICLLAGAASDCDCKNDVNCICYSGDDAYATDAILNSPSSLAVAPDGTIYIA 1551

QUERY: 1520 DLGNIRIRAVSKNKPVLNAFNQYEAASPGEQELYVFNADGIHQYTVSLVTGEYLYNFTYS 1579
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1552 DLGNIRIRAVSKNKPVLNAFNQYEAASPGEQELYVFNADGIHQYTVSLVTGEYLYNFTYS 1611

QUERY: 1580 TDNDVTELIDNNGNSLKIRRDSSGMPRHLLMPDNQIITLTVGTNGGLKVVSTQNLELGLM 1639
             ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
SBJCT: 1612 ADNDVTELIDNNGNSLKIRRDSSGMPRHLLMPDNQIITLTVGTNGGLKAVSTQNLELGLM 1671

QUERY: 1640 TYDGNTGLLATKSDETGWTTFYDYDHEGRLTNVTRPTGVVTSLHREMEKSITIDIENSNR 1699
            ||||||||||||||||||||||||||||||||||||||||||||||||||||+|||||||
SBJCT: 1672 TYDGNTGLLATKSDETGWTTFYDYDHEGRLTNVTRPTGVVTSLHREMEKSITVDIENSNR 1731

QUERY: 1700 DDDVTVITNLSSVEASYTVVQDQVRNSYQLCNNGTLRVMYANGMGISFHSEPHVLAGTIT 1759
            |+|||||||||||||||||||||||||||||+|||||||||||||+||||||||||||+|
SBJCT: 1732 DNDVTVITNLSSVEASYTVVQDQVRNSYQLCSNGTLRVMYANGMGVSFHSEPHVLAGTLT 1791

QUERY: 1760 PTIGRCNISLPMENGLNSIEWRLRKEQIKGKVTIFGRKLRVHGRNLLSIDYDRNIRTEKI 1819
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1792 PTIGRCNISLPMENGLNSIEWRLRKEQIKGKVTIFGRKLRVHGRNLLSIDYDRNIRTEKI 1851

QUERY: 1820 YDDHRKFTLRIIYDQVGRPFLWLPSSGLAAVNVSYFFNGRLAGLQRGAMSERTDIDKQGR 1879
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1852 YDDHRKFTLRIIYDQVGRPFLWLPSSGLAAVNVSYFFNGRLAGLQRGAMSERTDIDKQGR 1911

QUERY: 1880 IVSRMFADGKVWSYSYLDKSMVLLLQSQRQYIFEYDSSDRLLAVTMPSVARHSMSTHTSI 1939
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
SBJCT: 1912 IVSRMFADGKVWSYSYLDKSMVLLLQSQRQYIFEYDSSDRLHAVTMPSVARHSMSTHTSI 1971

QUERY: 1940 GYIRNIYNPPESNASVIFDYSDDGRILKTSFLGTGRQVFYKYGKLSKLSEIVYDSTAVTF 1999
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1972 GYIRNIYNPPESNASVIFDYSDDGRILKTSFLGTGRQVFYKYGKLSKLSEIVYDSTAVTF 2031

QUERY: 2000 GYDETTGVLKMVNLQSGGFSCTIRYRKIGPLVDKQIYRFSEEGMVNARFDYTYHDNSFRI 2059
            |||||||||||||||||||||||||||+||||||||||||||||+|||||||||||||||
SBJCT: 2032 GYDETTGVLKMVNLQSGGFSCTIRYRKVGPLVDKQIYRFSEEGMINARFDYTYHDNSFRI 2091

QUERY: 2060 ASIKPVISETPLPVDLYRYDEISGKVEHFGKFGVIYYDINQIITTAVMTLSKHFDTHGRI 2119
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2092 ASIKPVISETPLPVDLYRYDEISGKVEHFGKFGVIYYDINQIITTAVMTLSKHFDTHGRI 2151

QUERY: 2120 KEVQYEMFRSLMYWMTVQYDSMGRVIKRELKLGPYANTTKYTYDYDGDGQLQSVAVNDRP 2179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2152 KEVQYEMFRSLMYWMTVQYDSMGRVIKRELKLGPYANTTKYTYDYDGDGQLQSVAVNDRP 2211

QUERY: 2180 TWRYSYDXXXXXXXXXXXXXSVRLMPLRYDLRDRITRLGDVQYKIDDDGYLCQRGSDIFEY 2239
            |||||||             | ||||||||||||||||||||||||||||||||||||||
SBJCT: 2212 TWRYSYDLNGNLHLLNPGNSARLMPLRYDLRDRITRLGDVQYKIDDDGYLCQRGSDIFEY 2271

QUERY: 2240 NSKGLLTRAYNKASGWSVQYRYDGVGRRASYKTNLGHHLQYFYSDLHNPTRITHVYNHSN 2299
            |||||||||||||||||||||||| |||||||||||||||||||+|||||||||||
SBJCT: 2272 NSKGLLTRAYNKASGWSVQYRYDGVSRRASYKTNLGHHLQYFYSDLHHPTRITHVYNHSN 2331

QUERY: 2300 SEITSLYYDLQGHLFAMESSSGEEYYVASDNTGTPLAVFSINGLMIKQLQYTAYGEIYYD 2359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2332 SEITSLYYDLQGHLFAMESSSGEEYYVASDNTGTPLAVFSINGLMIKQLQYTAYGEIYYD 2391

QUERY: 2360 SNPDFQMVIGFHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWKNVGKEPAPFNLYMF 2419
            ||||||||||||||||||||||||||||||||||||||||||||+|||||||||||||
SBJCT: 2392 SNPDFQMVIGFHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWRNVGKEPAPFNLYMF 2451

QUERY: 2420 KSNNPLSSELDLKNYVTDVKSWLVMFGFQLSNIIPGFPRAKMYFVPPPYELSESQASENG 2479
            |+|||||+||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2452 KNNNPLSNELDLKNYVTDVKSWLVMFGFQLSNIIPGFPRAKMYFVPPPYELSESQASENG 2511

QUERY: 2480 QLITGVQQTTERHNQAFMALEGQVITKKLHASIREKAGHWFATTTPIIGKGIMFAIKEGR 2539
            ||||||||||||||||+|||||||+||||| ||||||||||||||||||||||||||||
SBJCT: 2512 QLITGVQQTTERHNQAFLALEGQVISKKLHAGIREKAGHWFATTTPIIGKGIMFAIKEGR 2571

QUERY: 2540 VTTGVSSIASEDSRKVASVLNNAYYLDKMHYSIEGKDTHYFVKIGSADGDLVTLGTTIGR 2599
            ||||||||||||||||||||||||||||||||||||||||||||+|||||||||||||||
SBJCT: 2572 VTTGVSSIASEDSRKVASVLNNAYYLDKMHYSIEGKDTHYFVKIGAADGDLVTLGTTIGR 2631

QUERY: 2600 KVLESGVNVTVSQPTLLVNGRTRRFTNIEFQYSTLLLSIRYGLTPDTLDEEKARVLDQAR 2659
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2632 KVLESGVNVTVSQPTLLVNGRTRRFTNIEFQYSTLLLSIRYGLTPDTLDEEKARVLDQAR 2691

QUERY: 2660 QRALGTAWAKEQQKARDGREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADSS 2719
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2692 QRALGTAWAKEQQKARDGREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADSS 2751

QUERY: 2720 SNIQFLRQNEMGKR 2733
            ||||||||||||||
SBJCT: 2752 SNIQFLRQNEMGKR 2765

* = FCTR3F DOES NOT CONTAIN THESE AMINO ACIDS
```

The amino acid sequences of the FCTR3bcde and f proteins were also found to have 2536 of 2774 amino acid residues (91%) identical to, and 2558 of 2774 residues (91%) positive with, the 2764 amino acid residue protein Odd Oz/ten-m homolog 2 (*Drosophila*) (GenBank Acc:NP_035986.2) (SEQ ID NO:65), shown in Table 3U.

Table 3U. BLASTP of FCTR3bcde and f against Odd Oz/ten-m homolog 2 (SEQ ID NO:65)

```
>GI|7657415|REF|NP_035986.2| ODD OZ/TEN-M HOMOLOG 2 (DROSOPHILA); ODD OZ/TEN-M HOMOLOG
3
            (DROSOPHILA) [MUS MUSCULUS]
 GI|4760778|DBJ|BAA77397.1| (AB025411) TEN-M2 [MUS MUSCULUS]
          LENGTH = 2764

 SCORE = 4996 BITS (12961), EXPECT = 0.0
```

IDENTITIES = 2536/2774 (91%), POSITIVES = 2558/2774 (91%), GAPS = 51/2774 (1%)

```
QUERY: 1     MDVKDRRHRSLTRGRCGKECRYTSSSLDSEDCRVPTQKSYSSSETLKAYDHDSRMHYGNR 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1     MDVKDRRHRSLTRGRCGKECRYTSSSLDSEDCRVPTQKSYSSSETLKAYDHDSRMHYGNR 60

QUERY: 61    VTDLIHRESDEFPRQGTNFTLAELGICEPSPHRSGYCSDMGILHQGYSLSTGSDADSDTE 120
             ||||+||||||| |||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 61    VTDLVHRESDEFSRQGTNFTLAELGICEPSPHRSGYCSDMGILHQGYSLSTGSDADSDTE 120

QUERY: 121   GGMSPEHAIRLWGRGIKSRRSSGLSSRENSALTLTXXXXXXXXXXXXGRXXXXXXXXXXX 180
             |||||||||||||||||||||||||||||||||||            ||
SBJCT: 121   GGMSPEHAIRLWGRGIKSRRSSGLSSRENSALTLTDSDNENKSDDDNGRPIPPTSSSSLL 180

QUERY: 181   XXXXXXXXHNPPPVSCQMPLLDSNTSHQIMDTNPDEEFSPNSYLLRACXXXXXXXXXXXX 240
                     ||||||||||||||||||||||||||||||||||||||||
SBJCT: 181   PSAQLPSSHNPPPVSCQMPLLDSNTSHQIMDTNPDEEFSPNSYLLRACSGPQQASSSGPP 240

QUERY: 241   NHHSQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXQIHAPAPAPNDLATTPESVQ 300
             |||||                                   ||||||||||||||||||||
SBJCT: 241   NHHSQSTLRPPLPPPHNHTLSHHHSSANSLNRNSLTNRRSQIHAPAPAPNDLATTPESVQ 300

QUERY: 301   LQDSWVLNSNVPLETRHFLFKXXXXXXXXXXXXXXXYPLTSGTVYTPPPRLLPRNTFSRK 360
             |||||||||||||||||||||               ||||||||||||||||||||||||
SBJCT: 301   LQDSWVLNSNVPLETRHFLFKTSSGSTPLFSSSSPGYPLTSGTVYTPPPRLLPRNTFSRK 360

QUERY: 361   AFKLKKPSKYCSWKCXXXXXXXXXXXXXXXXXYFI------------------------- 395
             |||||||||||||||                 |||
SBJCT: 361   AFKLKKPSKYCSWKCAALSAIAAALLLAILLAYFIAMHLLGLNWQLQPADGHTFNNGVRT 420

QUERY: 396   ----------------VPWSLKNSSIDSGEAEVGRRVTQEVPPGVFWRSQIHISQPQFLK 439
                             ||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 421   GLPGNDDVATVPSGGKVPWSLKNSSIDSGEAEVGRRVTQEVPPGVFWRSQIHISQPQFLK 480

QUERY: 440   FNISLGKDALFGVYIRRGLPPSHAQYDFMERLDGKEKWSVVESPRERRSIQTLVQNEAVF 499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 481   FNISLGKDALFGVYIRRGLPPSHAQYDFMERLDGKEKWSVVESPRERRSIQTLVQNEAVF 540

QUERY: 500   VQYLDVGLWHLAFYNDGKDKEMVSFNTVVLDSVQDCPRNCHGNGECVSGVCHCFPGFLGA 559
             |||||||||||||||||||||||||||||||||||||||||||||||||+||||||||||
SBJCT: 541   VQYLDVGLWHLAFYNDGKDKEMVSFNTVVLDSVQDCPRNCHGNGECVSGLCHCFPGFLGA 600

QUERY: 560   DCAKAACPVLCSGNGQYSKGTCQCYSGWKGAECDVPMNQCIDPSCGGHGSCIDGNCVCSA 619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||+|
SBJCT: 601   DCAKAACPVLCSGNGQYSKGTCQCYSGWKGAECDVPMNQCIDPSCGGHGSCIDGNCVCAA 660

QUERY: 620   GYKGEHCEEVDCLDPTCSSHGVCVNGECLCSPGWGGLNCELARVQCPDQCSGHGTYLPDT 679
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||+
SBJCT: 661   GYKGEHCEEVDCLDPTCSSHGVCVNGECLCSPGWGGLNCELARVQCPDQCSGHGTYLPDS 720

QUERY: 680   GLCSCDPNWMGPDCSVEVCSVDCGTHGVCIGGACRCEEGWTGAACDQRVCHPRCIEHGTC 739
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
SBJCT: 721   GLCSCDPNWMGPDCSV-VCSVDCGTHGVCIGGACRCEEGWTGAACDQRVCHPRCIEHGTC 779
                              *********
QUERY: 740   KDGKCECREGWNGEHCTIGRQTAGTETDGCPDLCNGNGRCTLGQNSWQCVCQTGWRGPGC 799
             |||||||||||||||||         ||||||||||||||||||||||||||||||||||
SBJCT: 780   KDGKCECREGWNGEHCTI---------DGCPDLCNGNGRCTLGQNSWQCVCQTGWRGPGC 830

QUERY: 800   NVAMETSCADNKDNEGDGLVDCLDPDCCLQSACQNSLLCRGSRDPLDIIQQGQTDWPAVK 859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 831   NVAMETSCADNKDNEGDGLVDCLDPDCCLQSACQNSLLCRGSRDPLDIIQQGQTDWPAVK 890

QUERY: 860   SFYDRIKLLAGKDSTHIIPGENPFNSSLVSLIRGQVVTTDGTPLVGVNVSFVKYPKYGYT 919
             ||||||||||||||||||||+||||||||||||||||| |||||||||||||||||||||
SBJCT: 891   SFYDRIKLLAGKDSTHIIPGDNPFNSSLVSLIRGQVVTMDGTPLVGVNVSFVKYPKYGYT 950

QUERY: 920   ITRQDGTFDLIANGGASLTLHFERAPFMSQERTVWLPWNSFYAMDTLVMKTEENSIPSCD 979
             |||||||||||||||++|||||||||||||||||||||||||||||||||||||||||||
SBJCT: 951   ITRQDGTFDLIANGGSALTLHFERAPFMSQERTVWLPWNSFYAMDTLVMKTEENSIPSCD 1010
```

```
QUERY: 980  LSGFVRPDPIIISSPLSTFFSAAPGQNPIVPETQVLHEEIELPGSNVKLRYLSSRTAGYK 1039
            ||||||||||||||||||||||+|  ||||||||||||||||||+|||||||||||||||
SBJCT: 1011 LSGFVRPDPIIISSPLSTFFSASPASNPIVPETQVLHEEIELPGTNVKLRYLSSRTAGYK 1070

QUERY: 1040 SLLKITMTQSTVPLNLIRVHLMVAVEGHLFQKSFQASPNLASTFIWDKTDAYGQRVYGLS 1099
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
SBJCT: 1071 SLLKITMTQSTVPLNLIRVHLMVAVEGHLFQKSFQASPNLAYTFIWDKTDAYGQRVYGLS 1130

QUERY: 1100 DAVVSVGFEYETCPSLILWEKRTALLQGFELDPSNLGGWSLDKHHILNVKSGILHKGTGE 1159
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
SBJCT: 1131 DAVVSVGFEYETCPSLILWEKRTALLQGFELDPSNLGGWSLDKHHTLNVKSGILHKGTGE 1190

QUERY: 1160 NQFLTQQPAIITSIMGNGRRRSISCPSCNGLAEGNKLLAPVALAVGIDGSLYVGDFNYIR 1219
            |||||||||||||||||||||||||||||||||||||||||||||||||||+||||||||
SBJCT: 1191 NQFLTQQPAIITSIMGNGRRRSISCPSCNGLAEGNKLLAPVALAVGIDGSLFVGDFNYIR 1250

QUERY: 1220 RIFPSRNVTSILELRNKEFKHSNNPAHKYYLAVDPVSGSLYVSDTNSRRIYRVKSLSGTK 1279
            |||||||||||||||||||||||+| ||||||||||+||||||||||||||||||||| |
SBJCT: 1251 RIFPSRNVTSILELRNKEFKHSNSPGHKYYLAVDPVTGSLYVSDTNSRRIYRVKSLSGAK 1310

QUERY: 1280 DLAGNSEVVAGTGEQCLPFDEARCGDGGKAIDATLMSPRGIAVDKNGLMYFVDATMIRKV 1339
            ||||||||||||||||||||||||||||||+|||||||||||||||||||||||||||||
SBJCT: 1311 DLAGNSEVVAGTGEQCLPFDEARCGDGGKAVDATLMSPRGIAVDKNGLMYFVDATMIRKV 1370

QUERY: 1340 DQNGIISTLLGSNDLTAVRPLSCDSSMDVAQVRLEWPTDLAVNPMDNSLYVLENNVILRI 1399
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1371 DQNGIISTLLGSNDLTAVRPLSCDSSMDVAQVRLEWPTDLAVNPMDNSLYVLENNVILRI 1430

QUERY: 1400 TENHQVSIIAGRPMHCQVPGIDYSLSKXXXXXXXXXXXXXXXXXTGVLYITETDEKKINR 1459
            |||||||||||||||||||||||||||                 ||||||||||||||||
SBJCT: 1431 TENHQVSIIAGRPMHCQVPGIDYSLSKLAIHSALESASAIAISHTGVLYITETDEKKINR 1490

QUERY: 1460 LRQVTTNGEICLLAGAASXXXXXXXXXXXXYSGDDAYATDAILNSPSSLAVAPDGTIYIA 1519
            ||||||||||||||||||            ||||||||||||||||||||||||||||||
SBJCT: 1491 LRQVTTNGEICLLAGAASDCDCKNDVNCICYSGDDAYATDAILNSPSSLAVAPDGTIYIA 1550

QUERY: 1520 DLGNIRIRAVSKNKPVLNAFNQYEAASPGEQELYVFNADGIHQYTVSLVTGEYLYNFTYS 1579
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1551 DLGNIRIRAVSKNKPVLNAFNQYEAASPGEQELYVFNADGIHQYTVSLVTGEYLYNFTYS 1610

QUERY: 1580 TDNDVTELIDNNGNSLKIRRDSSGMPRHLLMPDNQIITLTVGTNGGLKVVSTQNLELGLM 1639
             ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
SBJCT: 1611 ADNDVTELIDNNGNSLKIRRDSSGMPRHLLMPDNQIITLTVGTNGGLKAVSTQNLELGLM 1670

QUERY: 1640 TYDGNTGLLATKSDETGWTTFYDYDHEGRLTNVTRPTGVVTSLHREMEKSITIDIENSNR 1699
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1671 TYDGNTGLLATKSDETGWTTFYDYDHEGRLTNVTRPTGVVTSLHREMEKSITIDIENSNR 1730

QUERY: 1700 DDDVTVITNLSSVEASYTVVQDQVRNSYQLCNNGTLRVMYANGMGISFHSEPHVLAGTIT 1759
            |||||||||||||||||||||||||||||||||||||||||||| +||||||||||||||
SBJCT: 1731 DDDVTVITNLSSVEASYTVVQDQVRNSYQLCNNGTLRVMYANGMAVSFHSEPHVLAGTIT 1790

QUERY: 1760 PTIGRCNISLPMENGLNSIEWRLRKEQIKGKVTIFGRKLRVHGRNLLSIDYDRNIRTEKI 1819
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1791 PTIGRCNISLPMENGLNSIEWRLRKEQIKGKVTIFGRKLRVHGRNLLSIDYDRNIRTEKI 1850

QUERY: 1820 YDDHRKFTLRIIYDQVGRPFLWLPSSGLAAVNVSYFFNGRLAGLQRGAMSERTDIDKQGR 1879
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1851 YDDHRKFTLRIIYDQVGRPFLWLPSSGLAAVNVSYFFNGRLAGLQRGAMSERTDIDKQGR 1910

QUERY: 1880 IVSRMFADGKVWSYSYLDKSMVLLLQSQRQYIFEYDSSDRLLAVTMPSVARHSMSTHTSI 1939
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
SBJCT: 1911 IVSRMFADGKVWSYSYLDKSMVLLLQSQRQYIFEYDSSDRLHAVTMPSVARHSMSTHTSI 1970

QUERY: 1940 GYIRNIYNPPESNASVIFDYSDDGRILKTSFLGTGRQVFYKYGKLSKLSEIVYDSTAVTF 1999
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1971 GYIRNIYNPPESNASVIFDYSDDGRILKTSFLGTGRQVFYKYGKLSKLSEIVYDSTAVTF 2030

QUERY: 2000 GYDETTGVLKMVNLQSGGFSCTIRYRKIGPLVDKQIYRFSEEGMVNARFDYTYHDNSFRI 2059
            |||||||||||||||||||||||||+||||||||||||||||+|||||||||||||||||
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SBJCT: 2031 GYDETTGVLKMVNLQSGGFSCTIRYRKVGPLVDKQIYRFSEEGMINARFDYTYHDNSFRI 2090

QUERY: 2060 ASIKPVISETPLPVDLYRYDEISGKVEHFGKFGVIYYDINQIITTAVMTLSKHFDTHGRI 2119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2091 ASIKPVISETPLPVDLYRYDEISGKVEHFGKFGVIYYDINQIITTAVMTLSKHFDTHGRI 2150

QUERY: 2120 KEVQYEMFRSLMYWMTVQYDSMGRVIKRELKLGPYANTTKYTYDYDGDGQLQSVAVNDRP 2179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2151 KEVQYEMFRSLMYWMTVQYDSMGRVIKRELKLGPYANTTKYTYDYDGDGQLQSVAVNDRP 2210

QUERY: 2180 TWRYSYDXXXXXXXXXXXXXSVRLMPLRYDLRDRITRLGDVQYKIDDDGYLCQRGSDIFEY 2239
            |||||||             | |||||||||||||||||||||||||||||||||||||||
SBJCT: 2211 TWRYSYDLNGNLHLLNPGNSARLMPLRYDLRDRITRLGDVQYKIDDDGYLCQRGSDIFEY 2270

QUERY: 2240 NSKGLLTRAYNKASGWSVQYRYDGVGRRASYKTNLGHHLQYFYSDLHNPTRITHVYNHSN 2299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2271 NSKGLLTRAYNKASGWSVQYRYDGVGRRASYKTNLGHHLQYFYSDLHNPTRITHVYNHSN 2330

QUERY: 2300 SEITSLYYDLQGHLFAMESSSGEEYYVASDNTGTPLAVFSINGLMIKQLQYTAYGEIYYD 2359
            ||||||||||||||||||||||||||||||||||||||+|||||||||||||||||||||
SBJCT: 2331 SEITSLYYDLQGHLFAMESSSGEEYYVASDNTGTPLAVYSINGLMIKQLQYTAYGEIYYD 2390

QUERY: 2360 SNPDFQMVIGFHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWKNVGKEPAPFNLYMF 2419
            |||||||||||||||||||||||||||||||||||||||||||||+||||||||||||||
SBJCT: 2391 SNPDFQMVIGFHGGLYDPLTKLVHFTQRDYDVLAGRWTSPDYTMWRNVGKEPAPFNLYMF 2450

QUERY: 2420 KSNNPLSSELDLKNYVTDVKSWLVMFGFQLSNIIPGFPRAKMYFVPPPYELSESQASENG 2479
            |+|||||+||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2451 KNNNPLSNELDLKNYVTDVKSWLVMFGFQLSNIIPGFPRAKMYFVPPPYELSESQASENG 2510

QUERY: 2480 QLITGVQQTTERHNQAFMALEGQVITKKLHASIREKAGHWFATTTPIIGKGIMFAIKEGR 2539
            |||||||||||||||||+||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2511 QLITGVQQTTERHNQAFLALEGQVITKKLHASIREKAGHWFATTTPIIGKGIMFAIKEGR 2570

QUERY: 2540 VTTGVSSIASEDSRKVASVLNNAYYLDKMHYSIEGKDTHYFVKIGSADGDLVTLGTTIGR 2599
            ||||||||||||||||||||||||||||||||||||||||||||||+|||||||||||||
SBJCT: 2571 VTTGVSSIASEDSRKVASVLNNAYYLDKMHYSIEGKDTHYFVKIGAADGDLVTLGTTIGR 2630

QUERY: 2600 KVLESGVNVTVSQPTLLVNGRTRRFTNIEFQYSTLLLSIRYGLTPDTLDEEKARVLDQAR 2659
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2631 KVLESGVNVTVSQPTLLVNGRTRRFTNIEFQYSTLLLSIRYGLTPDTLDEEKARVLDQAG 2690

QUERY: 2660 QRALGTAWAKEQQKARDGREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADSS 2719
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 2691 QRALGTAWAKEQQKARDGREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADSS 2750

QUERY: 2720 SNIQFLRQNEMGKR 2733
            ||||||||||||||
SBJCT: 2751 SNIQFLRQNEMGKR 2764

* = FCTR3F DOES NOT CONTAIN THESE AMINO ACIDS
```

FCTR3 is related to rat neurestin, a gene implicated in neuronal development (Otaki JM, Firestein S Dev Biol 1999 Aug 1;212(1):165-81) Neurestin shows homology to human gamma-heregulin, a Drosophila receptor-type pair-rule gene product, Odd Oz (Odz) / Ten(m), and Ten(a). Neurestin has putative roles in synapse formation and brain morphogenesis. A mouse neurestin homolog, DOC4, has independently been isolated from the NIH-3T3 fibroblasts. DOC4 is also known as tenascin M (TNM), a *Drosophila* pair-rule gene homolog containing extracellular EGF-like repeats. The significant homology to these molecules and in particular, γ-heregulin, have important implications regarding the potential contribution of FCTR3 to disease progression. Heregulin is the ligand for HER-2/ErbB2/NEU, a proto-oncogene receptor tyrosine

kinase implicated in breast and prostate cancer progression that was originally identified in rat neuro/glioblastoma cell lines. Extopic expression of HER-2/ErbB2/NEU in MDA-MB-435 breast adenocarcinoma cells confers chemoresistance to Taxol-induced apoptosis relative to vector transfected control cells (Yu et al. Overexpression of ErbB2 blocks Taxol-induced apoptosis by up-regulation of p21Cip1, which inhibits p34Cdc2 kinase. Molec. Cell 2: 581-591, 1998).

FCTR3 related tenascins and cancer biology

As mentioned, FCTR3 also has significant homology to DOC4, (AKA tenascin M), a *Drosophila* pair-rule gene homolog containing extracellular EGF-like repeats. The tenascins are a growing family of extracellular matrix proteins that play prominent roles in tissue interactions critical to embryogenesis. Overexpression of tenascins has been described in multiple human solid malignancies.

The role of the tenascin family of related proteins is to regulate epithelial-stromal interactions, participate in fibronectin-dependent cell attachment and interaction. Indeed, tenascin-C (TN) is overexpressed in the stroma of malignant ovarian tumours particularly at the interface between epithelia and stroma leading to suggestions that it may be involved in the process of invasion (Wilson et al (1996) Br J Cancer 74: 999-1004). Tenascin-C is considered a therapeutic target for certain malignant brain tumors (Gladson CL : J Neuropathol Exp Neurol 1999 Oct;58(10):1029-40). Stromal or moderate to strong periductal Tenascin-C expression in DCIS (ductal carcinoma in situ) correlates with tumor cell invasion. (Jahkola et al. Eur J Cancer 1998 Oct;34(11):1687-92. Tenascin-C expression at the invasion border of early breast cancer is a useful predictor of local and distant recurrence. Jahkola T, et al. Br J Cancer. 1998 Dec;78(11):1507-13). Tenascin (TN) is an extracellular matrix protein found in areas of cell migration during development and expressed at high levels in migratory glioma cells. Treasurywala S, Berens ME Glia 1998 Oct;24(2):236-43 Migration arrest in glioma cells is dependent on the alphaV integrin subunit. Phillips GR, Krushel LA, Crossin KL J Cell Sci 1998 Apr;111 (Pt 8):1095-104 Domains of tenascin involved in glioma migration. Finally, tenascin expression in hormone-dependent tissues of breast and endometrium indicate that Tenascin expression reflects malignant progression and is down-regulated by antiprogestins during terminal differentiation of rat mammary tumors (Vollmer et al. Cancer Res 1992 Sep 1;52(17):4642-8)

Potential role of FCTR3 in oncologic disease progression:

Based on the bioactivity described in the medical literature for related molecules, FCTR3 may play a role in one or more aspects of tumor cell biology that alter the interactions of tumor epithelial cells with stromal components. In consideration, FCTR3 may play a role in the following malignant properties:

Autocrine/paracrine stimulation of tumor cell proliferation

Autocrine/paracrine stimulation of tumor cell survival and tumor cell resistance to cytotoxic therapy

Local tissue remodeling, paranechmal and basement membrane invasion and motility of tumor cells thereby contributing to metastasis.

Tumor-mediated immunosuppression of T-cell mediated immune effector cells and pathways resulting in tumor escape from immune surveilance.

Therapeutic intervention targeting FCTR3 in oncologic and central nervous system indications:

Predicted disease indications from expression profiling in 41 normal human tissues and 55 human cancer cell lines (see Example 2) include a subset of human gliomas, astrocytomas, mixed glioma/astrocytomas, renal cells carcinoma, breast adenocarcinoma, ovarian cancer, melanomas. Targeting of FCTR3 by human or humanized monoclonal antibodies designed to disrupt predicted interactions of FCTR3 with its cognate ligand may result in significant anti-tumor/anti-metastatic activity and the amelioration of associated symptomatology. Identification of small molecules that specifically/selectively interfere with downstream signaling components engaged by FCTR3/ligandinteractions would also be expected to result in significant anti-tumor/anti-metastatic activity and the amelioration of associated symptomatology. Likewise, modified antisense ribonucleotides or antisense gene expression constructs (plasmids, adenovirus, adeno-associated viruses, “naked” DNA approaches) designed to diminish the expression of FCTR3 transcripts/messenger RNA (mRNA) would be anticipated based on predicted properties of FCTR3 to have anti-tumor impact.

Based on the relatedness to neurestin and heregulins, as well as its high level expression in brain tissue, FCTR3 may also be used for remyelination in order to promote regeneration/repair/remyleination of injured central nervous system cells resulting from ischemia, brain trauma and various neurodegenerative diseases.. This postulate is based on reports indicating that neuregulin, glial growth factor 2, diminishes autoimmune demyelination and enhances remyelination in a chronic relapsing model for multiple sclerosis (Cannella et al. .

Proc. Nat. Acad. Sci. 95: 10100-10105, 1998). The expression of the related molecule neurestin can be induced in external tufted cells during regeneration of olfactory sensory neurons.

FCTR4

FCTR4 is a plasma membrane protein related to NF-Kappa-B P65delta3 protein. The clone is expressed in fetal liver tissues.

The novel FCTR4 nucleic acid of 609 nucleotides (also referred to as 29692275.0.1) is shown in Table 4A. An ORF begins with an ATG initiation codon at nucleotides 99-101 and ends with a TAA codon at nucleotides 522-524. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 4A, and the start and stop codons are in bold letters.

Table 4A. FCTR4 Nucleotide Sequence (SEQ ID NO:14)

```
CTGACATACTATATTAGTTGTTTGTTCACTGTCTCCACTCCAGCTAGAATATAAGTTCCATAGGGCAGAGTTTTTGTTCA
CTGCTATATTTTATAAGCATGAATGAATGCATGAACGAATGGACTGATAACCCACAAGCCAAAGACCTCCATGACCTGCC
ACTGCCCTCCTTTCATTTTATTCTCACCTCTACCAATACTAAATCACCTAGTTATGTAAATACGATATGCACTTTCATGG
CCCCTTGCTTTGTCATATGCTGTTCCCTTTGCCTGGAATATAAACTCTCAAAATACCATCCACATTTTAAAATCTTCTCC
AGAAAGCTTCCTCTGTCCACCCCCACCCTCCCACCCCCATATAGAGTAAGTCAGTCTTTCCTTTGTGCTACATTTGTACC
TGTATCTACAGTGGCTCTAATCAAACTGCACTGTGTCTCTCACTTCCTAGATTGTGAACTCTTTGAGGCTGAAGACTACT
TATTCATCTCTTTACCTCCAATGCCTAGGACAGGACCTTCATAAAGCAACTACTCTATAAATGTTGAAACATATGCATGA
CTATTCTGTAACAGGAATGAAAATATGGCATTTCAAGAAGTCACTACTC
```

The FCTR4 protein encoded by SEQ ID NO:14 has 141 amino acid residues and is presented using the one-letter code in Table 4B. The Psort profile for FCTR4 predicts that this sequence has no N-terminal signal peptide and is likely to be localized at the plasma membrane with a certainty of 0.6000. The most likely cleavage site for a peptide is between amino acids 39 and 40, *i.e.*, at the dash in the amino acid sequence ACT-CCA, based on the SignalP result. The predicted molecular weight of this protein is 16051.5 Daltons.

Table 4B. Encoded FCTR4 protein sequence (SEQ ID NO:15).

```
MNECMNEWTDNPQAKDLHDLPLPSFHFILTSTNTKSPSYVNTICTFMAPCFVICCSLCLEYKLSKYHPHFKIFSRKLPLSTPTLPP
PYRVSQSFLCATFVPVSTVALIKLHCVSHFLDCELFEAEDYLFISLPPMPRTGPS
```

The predicted amino acid sequence was searched in the publicly available GenBank database FCTR4 protein showed 30 % identities (22 over 72 amino acids) and 43% homologies (31over 72 amino acids) with hypothetical 10 kD protein of *Trypanosoma cru*zi (86 aa; ACC:Q99233) shown in Table 4C. The best homologies with a human protein were 54 % identities (114 over 343 amino acids) with NF-Kappa-B P65delta3 protein (71 aa fragment; ACC:Q13313) (SEQ ID NO:77).

Table 4C. BLASTP of FCTR4 against protein sequences

BLAST X search results are shown below:

ptnr:SPTREMBL-ACC:Q99233 HYPOTHETICAL 10 KD PROTEIN +3, 68, 0.60, 1, (SEQ ID

NO:73)

ptnr:SPTREMBL-ACC:Q16896 GABA RECEPTOR SUBUNIT - AEDES +3, 66, 0.81, 4 (SEQ ID NO:74)

ptnr:SPTREMBL-ACC:O76473 GABA RECEPTOR SUBUNIT - LEPTI... +3, 66, 0.99, 2 (SEQ ID NO:75)

ptnr:TREMBLNEW-ACC:AAD28317 F13J11.13 PROTEIN - Arabid... +3, 62, 0.99, 1 (SEQ ID NO:76)

Based upon homology, FCTR4 proteins and each homologous protein or peptide may share at least some activity.

FCTR5

FCTR5 is a protein bearing sequence homology to human complement C1R component precursor. The clone is expressed in breast, heart, lung, fetal lung, salivary gland, adrenal gland, spleen, kidney, and fetal kidney.

The novel FCTR5 nucleic acid of 1667 nucleotides (also referred to as 32125243.0.21) is shown in Table 5A. An ORF begins with an ATG initiation codon at nucleotides 34-36 and ends with a TGA codon at nucleotides 1495-1497. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 5A, and the start and stop codons are in bold letters.

Table 5A. FCTR5a Nucleotide Sequence (SEQ ID NO:16)

GTTCTCTCGCAGGTCCCAGATGTCCAGTTCCAG**ATG**CCTGGACCCAGAGTGTGGGGAAATATCTCTGGAGAAGCCCTCA
CTCCAAAGGCTGTCCAGGCGCAATGTGGTGGCTGCTTCTCTGGGGAGTCCTCCAGGCTTGCCCAACCCGGGGCTCCGTCC
TCTTGGCCCAAGAGCTACCCCAGCAGCTGACATCCCCCGGGTACCCAGAGCCGTATGGCAAAGGCCAAGAGAGCAGCACG
GACATCAAGGCTCCAGAGGGCTTTGCTGTGAGGCTCGTCTTCCAGGACTTCGACCTGGAGCCGTCCCAGGACTGTGCAGG
GGACTCTGTCACAATCTCATTCGTCGGTTCGGATCCAAGCCAGTTCTGTGGTCAGCAAGGCTCCCCTCTGGGCAGGCCCC
CTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGTTTGCGGCTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAGACT
GCCCACCTCCACAAGGGCTTCCTGGCCCTCTACCAAACCGTGGCTGTGAACTATAGTCAGCCCATCAGCGAGGCCAGCAG
GGGCTCTGAGGCCATCAACGCACCTGGAGACAACCCTGCCAAGGTCCAGAACCACTGCCAGGAGCCCTATTATCAGGCCG
CGGCAGCAGGGGCACTCACCTGTGCAACCCCAGGGACCTGGAAAGACAGACAGGATGGGGAGGAGGTTCTTCAGTGTATG
CCTGTCTGCGGACGGCCAGTCACCCCCATTGCCCAGAATCAGACGACCCTCGGTTCTTCCAGAGCCAAGCTGGGCAACTT
CCCCTGGCAAGCCTTCACCAGTATCCACGGCCGTGGGGGCGGGGCCCTGCTGGGGGACAGATGGATCCTCACTGCTGCCC
ACACCATCTACCCCAAGGACAGTGTTTCTCTCAGGAAGAACCAGAGTGTGAATGTGTTCTTGGGCCACACAGCCATAGAT
GAGATGCTGAAACTGGGGAACCACCCTGTCCACCGTGTCGTTGTGCACCCCGACTACCGTCAGAATGAGTCCCATAACTT
TAGCGGGGACATCGCCCTCCTGGAGCTGCAGCACAGCATCCCCCTGGGCCCCAACGTCCTCCCGGTCTGTCTGCCCGATA
ATGAGACCCTCTACCGCAGCGGCTTGTTGGGCTACGTCAGTGGGTTTGGCATGGAGATGGGCTGGCTAACTACTGAGCTG
AAGTACTCGAGGCTGCCTGTAGCTCCCAGGGAGGCCTGCAACGCCTGGCTCCAAAAGAGACAGAGACCCGAGGTGTTTTC
TGACAATATGTTCTGTGTTGGGGATGAGACGCAAAGGCACAGTGTCTGCCAGGGGGACAGTGGCAGCCTCTATGTGGTAT
GGGACAATCATGCCCATCACTGGGTGGCCACGGGCATTGTGTCCTGGGGCATAGGGTGTGGCGAAGGGTATGACTTCTAC
ACCAAGGTGCTCAGCTATGTGGACTGGATCAAGGGAGTGATGAATGGCAAGAAT**TGA**CCCTGGGGGCTTGAACAGGGACT
GACCAGCACAGTGGAGGCCCCAGGCAACAGAGGGCCTGGAGTGAGGACTGAACACTGGGGTAGGGGGTGGGGGTTTCTCT
TGCAGTGGCTTGGTGCAACAGTGATGTGAATAGGATTTCCCTTTTTTTTTTTTTTTTTAAAAAAAAA

The FCTR5 protein encoded by SEQ ID NO:16 has 487 amino acid residues, and is presented using the one-letter code in Table 5B. FCTR5 was searched against other databases using SignalPep and PSort search protocols. The FCTR5 protein is most likely microbody (peroxisome) (Certainty=0.6406) and seems to have no N-terminal signal sequence. The predicted molecular weight of FCTR5 protein is 53511.9 daltons.

Table 5B. Encoded FCTR5a protein sequence (SEQ ID NO:17).

```
MPGPRVWGKYLWRSPHSKGCPGAMWWLLLWGVLQACPTRGSVLLAQELPQQLTSPGYPEPYGKGQESSTDIKAPEGFAVRLVFQDF
DLEPSQDCAGDSVTISFVGSDPSQFCGQQGSPLGRPPGQREFVSSGRSLRLTFRTQPSSENKTAHLHKGFLALYQTVAVNYSQPIS
EASRGSEAINAPGDNPAKVQNHCQEPYYQAAAAGALTCATPGTWKDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRAKLGNFPW
QAFTSIHGRGGGALLGDRWILTAAHTIYPKDSVSLRKNQSVNVFLGHTAIDEMLKLGNHPVHRVVVHPDYRQNESHNFSGDIALLE
LQHSIPLGPNVLPVCLPDNETLYRSGLLGYVSGFGMEMGWLTTELKYSRLPVAPREACNAWLQKRQRPEVFSDNMFCVGDETQRHS
VCQGDSGSLYVVWDNHAHHWVATGIVSWGIGCGEGYDFYTKVLSYVDWIKGVMNGKN
```

An alternative embodiment, FCTR5b, is a 1691 base sequence shown in Table 5C.

Table 5C. FCTR5b Nucleotide Sequence (SEQ ID NO:18)

```
TTTTTTTTTAAAAAAAAAAAAAAAAAAGGGAAATCCTATTCACATCACTGTTGCACCAAGCCACTGCAAGAGAAACCCCCACCCCCT
ACCCCAGTGTTCAGTCCTCACTCCAGGCCCTCTGTTGCCTGGGGCCTCCACTGTGCTGGTCAGTCCCTGTTCAAGCCCCCAGGGTC
AATTCTTGCCATTCATCACTCCCTTGATCCAGTCCACATAGCTGAGCACCTTGGTGTAGAAGTCATACCCTTCGCCACACCCTATG
CCCCAGGACACAATGCCCGTGGCCACCCAGTGATGGGCATGATTGTCCCATACCACATAGAGGCTGCCACTGTCCCCCTGGCAGAC
ACTGTGCCTTTGCGTCTCATCCCCAACACAGAACATATTGTCAGAAAACACCTCGGGTCTCTGTCTCTTTTGGAGCCAGGCGTTGC
AGGCCTCCCTGGGAGCTACAGGCAGCCTCGAGTACTTCAGCTCAGTAGTTAGCCAGCCCATCTCCATGCCAAACCCACTGACGTAG
CCCAACAAGCCGCTGCGGTAGAGGGTCTCATTATCGGCAGACAGACCGGGAGGACGTTGGGGCCCAGGGGGATGCTGTGCTGCAG
CTCCAGGAGGGCGATGTCCCCGCTAAAGTTATGGGACTCATTCTGACGGTAGTCGGGGTGCACAACGACACGGTGGACAGGGTGGT
TCCCCAGTTTCAGCATCTCATCTATGGCTGTGTGGCCCAAGAACACATTCACACTCTGGTTCTTCCTGAGAGAAACACTGTCCTTG
GGGTAGATGGTGTGGGCAGCAGTGAGGATCCATCTGTCCCCCAGCAGGGCCCCGCCCCCACGGCCGTGGATACTGGTGAAGGCTTG
CCAGGGGAAGTTGCCCAGCTTGGCTCTGGAAGAACCGAGGGTCGTCTGATTCTGGGCAATGGGGGTGACTGGCCGTCCGCAGACAG
GCATACACTGAAGAACCTCCTCCCCATCCTGTCTGTCTTTCCAGGTCCCTGGGGTTGCACAGGTGAGTGCCCCTGCTGCCGCGGCC
TGATAATAGGGCTCCTGGCAGTGGTTCTGGACCTTGGCAGGGTTGTCTCCAGGTGCGTTGATGGCCTCAGAGCCCCTGCTGGCCTC
GCTGATGGGCTGACTATAGTTCACAGCCACGGTTTGGTAGAGGGCCAGGAAGCCCTTGTGGAGGTGGGCAGTCTTGTTCTCCGAGG
AAGGCTGTGTGCGGAAGGTCAGCCGCAAACTCCTCCCTGAGGATACAAACTCCCTCTGACCAGGGGGCCTGCCCAGAGGGGAGCCT
TGCTGACCACAGAACTGGCTTGGATCCGAACCGACGAATGAGATTGTGACAGAGTCCCCTGCACAGTCCTGGGACGGCTCCAGGTC
GAAGTCCTGGAAGACGAGCCTCACAGCAAAGCCCTCTGGAGCCTTGATGTCCGTGCTGCTCTCTTGGCCTTTGCCATACGGCTCTG
GGTACCCGGGGGATGTCAGCTGCTGGGGTAGCTCTTGGGCCAAGAGGACGGAGCCCCGGGTTGGGCAAGCCTGGAGGACTCCCCAG
AGAAGCAGCCACCACATTGCGCCTGGACAGCCTTTGGAGTGAGGGCTTCTCCAGAGATATTTCCCCCACACTCTGGGTCCAGGCAT
CTGGAACTGGACATCTGGGACCTGCGAGAGAACTGGCCCAGGATAGGGAACAAAAGG
```

The FCTR5b protein encoded by SEQ ID NO:18 has 487 amino acid residues, and is presented using the one-letter code in Table 5D. FCTR5 was searched against other databases using SignalPep and PSort search protocols. The FCTR5b protein is most likely microbody (peroxisome) (Certainty=0.6406) and seems to have no N-terminal signal sequence. The predicted molecular weight of FCTR5 protein is 53511.9 daltons.

Table 5D. Encoded FCTR5b protein sequence (SEQ ID NO:19).

```
MPGPRVWGKYLWRSPHSKGCPGAMWWLLLWGVLQACPTRGSVLLAQQLPQQLTSPGYPEPYGKGQESSTDIKAPEGFAVRLVFQDF
DLEPSQDCAGDSVTISFVGSDPSQFCGQQGSPLGRPPGQREFVSSGRSLRLTFRTQPSSENKTAHLHKGFLALYQTVAVNYSQPIS
EASRGSEAINAPGDNPAKVQNHCQEPYYQAAAAGALTCATPGTWKDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRAKLGNFPW
QAFTSIHGRGGGALLGDRWILTAAHTIYPKDSVSLRKNQSVNVFLGHTAIDEMLKLGNHPVHRVVVHPDYRQNESHNFSGDIALLE
LQHSIPLGPNVLPVCLPDNETLYRSGLLGYVSGFGMEMGWLTTELKYSRLPVAPREACNAWLQKRQRPEVFSDNMFCVGDETQRHS
VCQGDSGSLYVVWDNHAHHWVATGIVSWGIGCGEGYDFYTKVLSYVDWIKGVMNGKN
```

The predicted amino acid sequence was searched in the publicly available GenBank database FCTR5a protein showed 58 % identities (177 over 302 amino acids) and 74 % homologies (226 over 302 amino acids) with human complement C1R component precursor (EC 3.4.21.41) (705 aa.; ACC:P00736). Based upon homology, FCTR5 proteins and each homologous protein or peptide may share at least some activity.

In a search of sequence databases, it was found, for example, that the nucleic acid sequence the nucleotides 17-1594 of FCTR5a have 1575 of 1578 bases (99 %) identical to *Homo sapiens* complement C1r-like proteinase precursor (GENBANK-ID: XM_007061.1) (SEQ ID NO:78) (Table 5E).

Table 5E. BLASTN of FCTR5a against *Homo sapiens* complement C1r-like proteinase precursor (SEQ ID NO:78)

```
>GI|11436767|REF|XM_007061.1| HOMO SAPIENS COMPLEMENT C1R-LIKE PROTEINASE PRECURSOR,
(LOC51279),
            MRNA
          LENGTH = 3318

 SCORE = 3104 BITS (1566), EXPECT = 0.0
 IDENTITIES = 1575/1578 (99%)
 STRAND = PLUS / PLUS

QUERY: 17    CAGATGTCCAGTTCCAGATGCCTGGACCCAGAGTGTGGGGAAATATCTCTGGAGAAGCC 76
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1     CAGATGTCCAGTTCCAGATGCCTGGACCCAGAGTGTGGGGAAATATCTCTGGAGAAGCC 60

QUERY: 77    CTCACTCCAAAGGCTGTCCAGGCGCAATGTGGTGGCTGCTTCTCTGGGGAGTCCTCCAGG 136
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 61    CTCACTCCAAAGGCTGTCCAGGCGCAATGTGGTGGCTGCTTCTCTGGGGAGTCCTCCAGG 120

QUERY: 137   CTTGCCCAACCCGGGGCTCCGTCCTCTTGGCCCAAGAGCTACCCCAGCAGCTGACATCCC 196
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 121   CTTGCCCAACCCGGGGCTCCGTCCTCTTGGCCCAAGAGCTACCCCAGCAGCTGACATCCC 180

QUERY: 197   CCGGGTACCCAGAGCCGTATGGCAAAGGCCAAGAGAGCAGCACGGACATCAAGGCTCCAG 256
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 181   CCGGGTACCCAGAGCCGTATGGCAAAGGCCAAGAGAGCAGCACGGACATCAAGGCTCCAG 240

QUERY: 257   AGGGCTTTGCTGTGAGGCTCGTCTTCCAGGACTTCGACCTGGAGCCGTCCCAGGACTGTG 316
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 241   AGGGCTTTGCTGTGAGGCTCGTCTTCCAGGACTTCGACCTGGAGCCGTCCCAGGACTGTG 300

QUERY: 317   CAGGGGACTCTGTCACAATCTCATTCGTCGGTTCGGATCCAAGCCAGTTCTGTGGTCAGC 376
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 301   CAGGGGACTCTGTCACAATCTCATTCGTCGGTTCGGATCCAAGCCAGTTCTGTGGTCAGC 360

QUERY: 377   AAGGCTCCCCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGTT 436
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 361   AAGGCTCCCCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGTT 420

QUERY: 437   TGCGGCTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAGACTGCCCACCTCCACAAGG 496
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 421   TGCGGCTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAGACTGCCCACCTCCACAAGG 480

QUERY: 497   GCTTCCTGGCCCTCTACCAAACCGTGGCTGTGAACTATAGTCAGCCCATCAGCGAGGCCA 556
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 481   GCTTCCTGGCCCTCTACCAAACCGTGGCTGTGAACTATAGTCAGCCCATCAGCGAGGCCA 540

QUERY: 557   GCAGGGGCTCTGAGGCCATCAACGCACCTGGAGACAACCCTGCCAAGGTCCAGAACCACT 616
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
SBJCT:  541 GCAGGGGCTCTGAGGCCATCAACGCACCTGGAGACAACCCTGCCAAGGTCCAGAACCACT 600

QUERY:  617 GCCAGGAGCCCTATTATCAGGCCGCGGCAGCAGGGGCACTCACCTGTGCAACCCCAGGGA 676
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT:  601 GCCAGGAGCCCTATTATCAGGCCGCGGCAGCAGGGGCACTCACCTGTGCAACCCCAGGGA 660

QUERY:  677 CCTGGAAAGACAGACAGGATGGGGAGGAGGTTCTTCAGTGTATGCCTGTCTGCGGACGGC 736
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT:  661 CCTGGAAAGACAGACAGGATGGGGAGGAGGTTCTTCAGTGTATGCCTGTCTGCGGACGGC 720

QUERY:  737 CAGTCACCCCCATTGCCCAGAATCAGACGACCCTCGGTTCTTCCAGAGCCAAGCTGGGCA 796
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT:  721 CAGTCACCCCCATTGCCCAGAATCAGACGACCCTCGGTTCTTCCAGAGCCAAGCTGGGCA 780

QUERY:  797 ACTTCCCCTGGCAAGCCTTCACCAGTATCCACGGCCGTGGGGGCGGGGCCCTGCTGGGGG 856
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT:  781 ACTTCCCCTGGCAAGCCTTCACCAGTATCCACGGCCGTGGGGGCGGGGCCCTGCTGGGGG 840

QUERY:  857 ACAGATGGATCCTCACTGCTGCCCACACCATCTACCCCAAGGACAGTGTTTCTCTCAGGA 916
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
SBJCT:  841 ACAGATGGATCCTCACTGCTGCCCACACCGTCTACCCCAAGGACAGTGTTTCTCTCAGGA 900

QUERY:  917 AGAACCAGAGTGTGAATGTGTTCTTGGGCCACACAGCCATAGATGAGATGCTGAAACTGG 976
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT:  901 AGAACCAGAGTGTGAATGTGTTCTTGGGCCACACAGCCATAGATGAGATGCTGAAACTGG 960

QUERY:  977 GGAACCACCCTGTCCACCGTGTCGTTGTGCACCCCGACTACCGTCAGAATGAGTCCCATA 1036
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT:  961 GGAACCACCCTGTCCACCGTGTCGTTGTGCACCCCGACTACCGTCAGAATGAGTCCCATA 1020

QUERY: 1037 ACTTTAGCGGGGACATCGCCCTCCTGGAGCTGCAGCACAGCATCCCCCTGGGCCCCAACG 1096
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1021 ACTTTAGCGGGGACATCGCCCTCCTGGAGCTGCAGCACAGCATCCCCCTGGGCCCCAACG 1080

QUERY: 1097 TCCTCCCGGTCTGTCTGCCCGATAATGAGACCCTCTACCGCAGCGGCTTGTTGGGCTACG 1156
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1081 TCCTCCCGGTCTGTCTGCCCGATAATGAGACCCTCTACCGCAGCGGCTTGTTGGGCTACG 1140

QUERY: 1157 TCAGTGGGTTTGGCATGGAGATGGGCTGGCTAACTACTGAGCTGAAGTACTCGAGGCTGC 1216
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1141 TCAGTGGGTTTGGCATGGAGATGGGCTGGCTAACTACTGAGCTGAAGTACTCGAGGCTGC 1200

QUERY: 1217 CTGTAGCTCCCAGGGAGGCCTGCAACGCCTGGCTCCAAAAGAGACAGAGACCCGAGGTGT 1276
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1201 CTGTAGCTCCCAGGGAGGCCTGCAACGCCTGGCTCCAAAAGAGACAGAGACCCGAGGTGT 1260

QUERY: 1277 TTTCTGACAATATGTTCTGTGTTGGGGATGAGACGCAAAGGCACAGTGTCTGCCAGGGGG 1336
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1261 TTTCTGACAATATGTTCTGTGTTGGGGATGAGACGCAAAGGCACAGTGTCTGCCAGGGGG 1320

QUERY: 1337 ACAGTGGCAGCCTCTATGTGGTATGGGACAATCATGCCCATCACTGGGTGGCCACGGGCA 1396
            ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1321 ACAGTGGCAGCGTCTATGTGGTATGGGACAATCATGCCCATCACTGGGTGGCCACGGGCA 1380

QUERY: 1397 TTGTGTCCTGGGGCATAGGGTGTGGCGAAGGGTATGACTTCTACACCAAGGTGCTCAGCT 1456
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1381 TTGTGTCCTGGGGCATAGGGTGTGGCGAAGGGTATGACTTCTACACCAAGGTGCTCAGCT 1440

QUERY: 1457 ATGTGGACTGGATCAAGGGAGTGATGAATGGCAAGAATTGACCCTGGGGGCTTGAACAGG 1516
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1441 ATGTGGACTGGATCAAGGGAGTGATGAATGGCAAGAATTGACCCTGGGGGCTTGAACAGG 1500

QUERY: 1517 GACTGACCAGCACAGTGGAGGCCCCAGGCAACAGAGGGCCTGGAGTGAGGACTGAACACT 1576
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1501 GACTGACCAGCACAGTGGAGGCCCCAGGCAACAGAGGGCCTGGAGTGAGGACTGAACACT 1560

QUERY: 1577 GGGGTAGGGGGTGGGGT 1594
            |||||||||| ||||||
SBJCT: 1561 GGGGTAGGGGTTGGGGT 1578
```

In this search it was also found that the FCTR5a nucleic acid had homology to three fragments of *Homo sapiens* complement component 1, r subcomponent. It has 102 of 117 bases (87%) identical to 1458-1574, 82 of 94 bases (87%) identical to 2052-2145, and 54 of 63 bases (85%) identical to 1678-1740 all fragments of *Homo sapiens* complement component 1, r subcomponent (GenBank Acc: NM_001733.1) (Table 5F).

Table 5F. BLASTN of FCTR5a against *Homo sapiens* complement component 1, r subcomponent (SEQ ID NO:79)

```
>GI|4502492|REF|NM_001733.1| HOMO SAPIENS COMPLEMENT COMPONENT 1, R SUBCOMPONENT
(C1R), MRNA
          LENGTH = 2386

 SCORE =  113 BITS (57), EXPECT = 3E-22
 IDENTITIES = 102/117 (87%)
 STRAND = PLUS / PLUS

QUERY: 783   AGCCAAGCTGGGCAACTTCCCCTGGCAAGCCTTCACCAGTATCCACGGCCGTGGGGGCGG 842
             ||||||| ||||||||||||||||||| |  |||||||  |||||||| || ||||||||
SBJCT: 1458  AGCCAAGATGGGCAACTTCCCCTGGCAGGTGTTCACCAACATCCACGGGCGCGGGGGCGG 1517

QUERY: 843   GGCCCTGCTGGGGGACAGATGGATCCTCACTGCTGCCCACACCATCTACCCCAAGGA 899
             |||||||||||| ||| | ||||||||||| |||||||||||| | || ||||||||
SBJCT: 1518  GGCCCTGCTGGGCGACCGCTGGATCCTCACAGCTGCCCACACCCTGTATCCCAAGGA 1574


 SCORE = 91.7 BITS (46), EXPECT = 1E-15
 IDENTITIES = 82/94 (87%)
 STRAND = PLUS / PLUS

QUERY: 1380  CTGGGTGGCCACGGGCATTGTGTCCTGGGGCATAGGGTGTGGCGAAGGGTATGACTTCTA 1439
             |||||||||||||||||| |||||||||||||| |||||  ||   || |||| ||||||
SBJCT: 2052  CTGGGTGGCCACGGGCATCGTGTCCTGGGGCATCGGGTGCAGCAGGGGCTATGGCTTCTA 2111

QUERY: 1440  CACCAAGGTGCTCAGCTATGTGGACTGGATCAAG 1473
             |||||| ||||||| ||| |||||||||||||||
SBJCT: 2112  CACCAAAGTGCTCAACTACGTGGACTGGATCAAG 2145


 SCORE = 54.0 BITS (27), EXPECT = 2E-04
 IDENTITIES = 54/63 (85%)
 STRAND = PLUS / PLUS

QUERY: 1006  CACCCCGACTACCGTCAGAATGAGTCCCATAACTTTAGCGGGGACATCGCCCTCCTGGAG 1065
             ||||| |||||||||||| |||||||| | || |||   |||||||||||||| ||||||
SBJCT: 1678  CACCCGGACTACCGTCAGGATGAGTCCTACAATTTTGAGGGGGACATCGCCCTGCTGGAG 1737

QUERY: 1066  CTG 1068
             |||
SBJCT: 1738  CTG 1740
```

The amino acid sequence of the protein of FCTR5a 485 of 487 amino acid residues (99%) identical to, and 487 of 487 residues (100%) positive with, the 487 amino acid complement C1r-like proteinase precursor from *Homo sapiens* (GenBank-ACC: AAF44349.1) (SEQ ID NO:80) (Table 5G).

Table 5G. BLASTP of FCTR5a and b against Complement C1R-like proteinase precursor (SEQ ID NO:80)

```
>GI|7706083|REF|NP_057630.1| COMPLEMENT C1R-LIKE PROTEINASE PRECURSOR, [HOMO SAPIENS]
 GI|11436768|REF|XP_007061.1| COMPLEMENT C1R-LIKE PROTEINASE PRECURSOR, [HOMO SAPIENS]
 GI|7271475|GB|AAF44349.1|AF178985_1 (AF178985) COMPLEMENT C1R-LIKE PROTEINASE
PRECURSOR [HOMO SAPIENS]
          LENGTH = 487

 SCORE =  972 BITS (2513), EXPECT = 0.0
 IDENTITIES = 485/487 (99%), POSITIVES = 487/487 (100%)
                                                         R
QUERY: 1    MPGPRVWGKYLWRSPHSKGCPGAMWWLLLWGVLQACPTRGSVLLAQELPQQLTSPGYPEP 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1    MPGPRVWGKYLWRSPHSKGCPGAMWWLLLWGVLQACPTRGSVLLAQELPQQLTSPGYPEP 60

QUERY: 61   YGKGQESSTDIKAPEGFAVRLVFQDFDLEPSQDCAGDSVTISFVGSDPSQFCGQQGSPLG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 61   YGKGQESSTDIKAPEGFAVRLVFQDFDLEPSQDCAGDSVTISFVGSDPSQFCGQQGSPLG 120

QUERY: 121  RPPGQREFVSSGRSLRLTFRTQPSSENKTAHLHKGFLALYQTVAVNYSQPISEASRGSEA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 121  RPPGQREFVSSGRSLRLTFRTQPSSENKTAHLHKGFLALYQTVAVNYSQPISEASRGSEA 180

QUERY: 181  INAPGDNPAKVQNHCQEPYYQAAAAGALTCATPGTWKDRQDGEEVLQCMPVCGRPVTPIA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 181  INAPGDNPAKVQNHCQEPYYQAAAAGALTCATPGTWKDRQDGEEVLQCMPVCGRPVTPIA 240

QUERY: 241  QNQTTLGSSRAKLGNFPWQAFTSIHGRGGGALLGDRWILTAAHTIYPKDSVSLRKNQSVN 300
            ||||||||||||||||||||||||||||||||||||||||||||+|||||||||||||||
SBJCT: 241  QNQTTLGSSRAKLGNFPWQAFTSIHGRGGGALLGDRWILTAAHTVYPKDSVSLRKNQSVN 300

QUERY: 301  VFLGHTAIDEMLKLGNHPVHRVVVHPDYRQNESHNFSGDIALLELQHSIPLGPNVLPVCL 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 301  VFLGHTAIDEMLKLGNHPVHRVVVHPDYRQNESHNFSGDIALLELQHSIPLGPNVLPVCL 360

QUERY: 361  PDNETLYRSGLLGYVSGFGMEMGWLTTELKYSRLPVAPREACNAWLQKRQRPEVFSDNMF 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 361  PDNETLYRSGLLGYVSGFGMEMGWLTTELKYSRLPVAPREACNAWLQKRQRPEVFSDNMF 420

QUERY: 421  CVGDETQRHSVCQGDSGSLYVVWDNHAHHWVATGIVSWGIGCGEGYDFYTKVLSYVDWIK 480
            ||||||||||||||||||+|||||||||||||||||||||||||||||||||||||||||
SBJCT: 421  CVGDETQRHSVCQGDSGSVYVVWDNHAHHWVATGIVSWGIGCGEGYDFYTKVLSYVDWIK 480

QUERY: 481  GVMNGKN 487
            |||||||
SBJCT: 481  GVMNGKN 487

R = AT RESIDUE 46, FCTR5B DIFFERS FROM FCTR5A IN THAT Q46R. THE REST OF THE HOMOLOGY
IS THE SAME.
```

The full amino acid sequence of the protein of FCTR5a has 175 of 303 amino acid residues (58%) identical to, and 226 of 303 residues (74%) positive with the 400-701 amino acid segment, 72 of 157 residues (45%) identical and 94 of 157 residues (59%) positive with amino acids 1-155, and 36 of 139 residues (25%) identical and 58 of 139 residues (40%) positive with amino acids 188-312 of the 705 amino acid Complement C1R Component Precursor from *Homo sapiens* (GenBank-ACC: AAA51851.1) (SEQ ID NO:43) (Table 5H).

Table 5H. BLASTP of FCTR5a and b against Complement C1R Component Precursor (SEQ ID NO:81)

```
>GI|115204|SP|P00736|C1R_HUMAN COMPLEMENT C1R COMPONENT PRECURSOR
 GI|67614|PIR||C1HURB COMPLEMENT SUBCOMPONENT C1R (EC 3.4.21.41) PRECURSOR - HUMAN
 GI|179644|GB|AAA51851.1| (M14058) HUMAN COMPLEMENT C1R [HOMO SAPIENS]
          LENGTH = 705

 SCORE =  361 BITS (928), EXPECT = 8E-99
 IDENTITIES = 175/303 (58%), POSITIVES = 226/303 (74%), GAPS = 9/303 (2%)

QUERY: 189 AKVQNHCQEPYYQ--------AAAAGALTCATPGTWKDRQDGEEVLQCMPVCGRPVTPIA 240
           |++| +| ||||+                |  ||   | ||+ | ||++ +|+||||+|| |+
SBJCT: 400 ARIQYYCHEPYYKMQTRAGSRESEQGVYTCTAQGIWKNEQKGEKIPRCLPVCGKPVNPVE 459

QUERY: 241 QNQTTLGSSRAKLGNFPWQAFTSIHGRGGGALLGDRWILTAAHTIYPKDSVSLRKNQSVN 300
           | |  +|  +||+|||||| ||+||||||||||||||||||||||+|||+  + + | |++
SBJCT: 460 QRQRIIGGQKAKMGNFPWQVFTNIHGRGGGALLGDRWILTAAHTLYPKEHEA-QSNASLD 518

QUERY: 301 VFLGHTAIDEMLKLGNHPVHRVVVHPDYRQNESHNFSGDIALLELQHSIPLGPNVLPVCL 360
           |||||| ++|++||||||+ || ||||||+||+|| ||||||||++|+ ||||+||+||
SBJCT: 519 VFLGHTNVEELMKLGNHPIRRVSVHPDYRQDESYNFEGDIALLELENSVTLGPNLLPICL 578

QUERY: 361 PDNETLYRSGLLGYVSGFGMEMGWLTTELKYSRLPVAPREACNAWLQKRQRPEVFSDNMF 420
           |||+| |  ||+|||||||+    +  +|++ |||||   +||  ||+ + | +||| |||
SBJCT: 579 PDNDTFYDLGLMGYVSGFGVMEEKIAHDLRFVRLPVANPQACENWLRGKNRMDVFSQNMF 638

QUERY: 421 CVGDETQRHSVCQGDSGSLYVVWDNHAHHWVATGIVSWGIGCGEGYDFYTKVLSYVDWIK 480
           | |  + +   |||||| ++ | | +    |||||||||||||  || ||||||+||||||
SBJCT: 639 CAGHPSLKQDACQGDSGGVFAVRDPNTDRWVATGIVSWGIGCSRGYGFYTKVLNYVDWIK 698

QUERY: 481 GVM 483
             |
SBJCT: 699 KEM 701


 SCORE =  122 BITS (306), EXPECT = 1E-26
 IDENTITIES = 72/157 (45%), POSITIVES = 94/157 (59%), GAPS = 3/157 (1%)
                                     R
QUERY: 24  MWWLLLWGVLQACPTRGSVLLAQELPQQLTSPGYPEPYGKGQESSTDIKAPEGFAVRLVF 83
           || | |       |    ||+ + |+|  ++||| +|+||     |++| |   | |+ |+|||
SBJCT: 1   MWLLYLLVPALFCRAGGSIPIPQKLFGEVTSPLFPKPYPNNFETTTVITVPTGYRVKLVF 60

QUERY: 84  QDFDLEPSQDCAGDSVTISFVGSDPSQFCGQQGSPLGRPPGQREFVSSGRSLRLTFRTQP 143
           | ||||||+ |   | | ||        +|||| ||||| |||++||+|  |   + ||| |
SBJCT: 61  QQFDLEPSEGCFYDYVKISADKKSLGRFCGQLGSPLGNPPGKKEFMSQGNKMLLTFHTDF 120

QUERY: 144 SS-ENKTAHLHKGFLALYQTVAVNYSQPISEASRGSE 179
           |+ || |   +||||| ||  ||+  +   | +   | |
SBJCT: 121 SNEENGTIMFYKGFLAYYQ--AVDLDECASRSKSGEE 155


 SCORE = 36.3 BITS (83), EXPECT = 0.93
 IDENTITIES = 36/139 (25%), POSITIVES = 58/139 (40%), GAPS = 17/139 (12%)
                              R
QUERY: 35  ACPTRGSVLLAQELPQQLTSPGYPEPYGKGQESSTDIKAPEGFAVRLVF-QDFDLEPSQD 93
           +|     |  |  |     ++|  || |          +  |+    |  + | | + ||++  |
SBJCT: 188 SCQAECSSELYTEASGYISSLEYPRSYPPDLRCNYSIRVERGLTLHLKFLEPFDIDDHQQ 247

QUERY: 94  --CAGDSVTISFVGSDPSQFCGQQGSPLGRPPGQREFVSSGRSLRLTFRTQPSSENKTAH 151
             |  | + |   | +  +|||+|      |||   +  +|  ++ | | |   | ++
SBJCT: 248 VHCPYDQLQIYANGKNIGEFCGKQ-----RPP---DLDTSSNAVDLLFFTDESGDS---- 295

QUERY: 152 LHKGFLALYQTVAVNYSQP 170
             +|+    | |  +   ||
SBJCT: 296 --RGWKLRYTTEIIKCPQP 312
```

R = AT RESIDUE 46, FCTR5B DIFFERS FROM FCTR5A IN THAT Q46R. THE REST OF THE HOMOLOGY IS THE SAME.

Based upon homology, FCTR5 proteins and each homologous protein or peptide may share at least some activity.

FCTR6

The novel nucleic acid of 1078 nucleotides FCTR6a (also designated 27455183.0.19) encoding a novel human blood coagulation factor XI-like protein is shown in Table 6A. An ORF was identified beginning with an ATG initiation codon at nucleotides 243-245 and ending with a TAA codon at nucleotides 1044-1046. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 6A, and the start and stop codons are in bold letters.

Table 6A FCTR6a Nucleotide Sequence (SEQ ID NO:20)

TTGATCCGTGCCAAGTGGCTTTTTGTGGGCTCTGTAGAGTGCTCTAAACCCAGCTCGGCCTTTGCTGTATTAGACAGAAGCACCTC
ATTCATATCCCTGGGGCCCCTGATGGTGCAGTGGTCTGGCTGTGGTCTGCACACCAGCTATTCTGTTTTGTTTTGTTTTGTTTTTT
TCCTACCTTTTTCCAATCCTCACACCTTCTGATCAACAGCCCCAGTAGGGTTTAAAGGTCCTAGAGCTAC**ATG**GGATTTAGGTTTC
TGGGCACAGCCAATTCTGCCACTTTTGAGACTTCCCTTCCCCTTCCACTTGCCCCTCTCTGGTTCTCTGCCACCAGTCCAGAAGAA
CTGAGTGTCGTGCTGGGGACCAACGACTTAACTAGCCCATCCATGGAAATAAAGGAGGTCGCCAGCATCATTCTTCACAAAGACTT
TAAGAGAGCCAACATGGACAATGACATTGCCTTGCTGCTGCTGGCTTCGCCCATCAAGCTCGATGACCTGAAGGTGCCCATCTGCC
TCCCCACGCAGCCCGGCCCTGCCACATGGCGCGAATGCTGGGTGGCAGGTTGGGGCCAGACCAATGCTGCTGACAAAAACTCTGTG
AAAACGGATCTGATGAAAGTGCCAATGGTCATCATGGACTGGGAGGAGTGTTCAAAGATGTTTCCAAAACTTACCAAAAATATGCT
GTGTGCCGGATACAAGAATGAGAGCTATGATGCCTGCAAGGGTGACAGTGGGGGGCCTCTGGTCTGCACCCCAGAGCCTGGTGAGA
AGTGGTACCAGGTGGGCATCATCAGCTGGGGAAAGAGCTGTGGAGATAAGAACACCCCAGGGATATACACCTCGTTGGTGAACTAC
AACCTCTGGATCGAGAAAGTGACCCAGCTAGGAGGCAGGCCCTTCAATGCAGAGAAAAGGAGGACTTCTGTCAAACAGAAACCTAT
GGGCTCCCCAGTCTCGGGAGTCCCAGAGCCAGGCAGCCCCAGATCCTGGCTCCTGCTCTGTCCCCTGTCCCATGTGTTGTTCAGAG
CTATTTTGTAC**TGA**TAATAAAATAGAGGCTATTCTTTCAACCGAAA

The FCTR6a protein encoded by SEQ ID NO:20 has 267 amino acid residues and is presented using the one-letter code in Table 6B. FCTR6a was searched against other databases using SignalPep and PSort search protocols. The FCTR6a protein is most likely mitochondrial matrix space (Certainty= 0.4372) and seems to have no N-terminal signal sequence. The predicted molecular weight of FCTR6a protein is 29412.8 daltons.

Table 6B. Encoded FCTR6a protein sequence (SEQ ID NO:21).

MGFRFLGTANSATFETSLPLPLAPLWFSATSPEELSVVLGTNDLTSPSMEIKEVASIILHKDFKRANMDNDIALLLLASPIKLDDL
KVPICLPTQPGPATWRECWVAGWGQTNAADKNSVKTDLMKVPMVIMDWEECSKMFPKLTKNMLCAGYKNESYDACKGDSGGPLVCT
PEPGEKWYQVGIISWGKSCGDKNTPGIYTSLVNYNLWIEKVTQLGGRPFNAEKRRTSVKQKPMGSPVSGVPEPGSPRSWLLLCPLS
HVLFRAILY

In an alternative embodiment, FCTR6b (alternatively referred to as 27455183.0.145) has the 1334 residue sequence shown in Table 6C. An ORF was identified beginning with an ATG initiation codon at nucleotides 499-501 and ending with a TAA codon at nucleotides 1300-1302. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 6C, and the start and stop codons are in bold letters.

Table 6C FCTR6b Nucleotide Sequence (SEQ ID NO:22)

GATTTTAGAAGGTTAATCAAAAACCCGGGGACAGTTTCTTCATGGCATAACCACAGACCTTTGTGGCACCCGCTGT
CGTGGGATATCAAATATCCTCTGGGGTTCGGAATGTGGGCTTATTACTGAAGATCCTGTCTGCTTGGTCAGTGGCAGGTC
TAGACTAACTTCTGGTCCTGAGTTTCTAAAGTGCTGGTAGACCAGTTGATACAAAACAGATATAATAATGAATGCCTTAT
CTATCTGAAGGTCAGTTTGATCCGTGCCAAGTGGCTTTTTGTGGGCTGTGTAGAGTGCTCTAAACCCAGCTCGGCCTTTG
CTGTATTAGACAGAAGCACCTCATTCATATCCCTGGGGCCCCTGATGGTGCAGTGGTCTGGCTGTGGTCTGCACACCAGC
TATTCTGTTTTGTTTTGTTTTGTTTTGTTTTTTCCTACCTTTTTCCAATCCTCACACCTTCTGATCAACAGCCCCAGTAG
GGTTTAAAGGTCCTAGAGCTAC**ATG**GGATTTAGGTTTCTGGGCACAGCCAATTCTGCCACTTTTGAGACTTCCCTTCCCC
TTCCACTTGCCCCTCTCTGGTTCTCTGCCACCAGTCCAGAAGAACTGAGTGTCGTGCTGGGGACCAACGACTTAACTAGC
CCATCCATGGAAATAAAGGAGGTCGCCAGCATCATTCTTCACAAAGACTTTAAGAGAGCCAACATGGACAATGACATTGC
CTTGCTGCTGCTGGCTTCGCCCATCAAGCTCGATGACCTGAAGGTGCCCATCTGCCTCCCCACGCAGCCCGGCCCTGCCA
CATGGCGCGAATGCTGGGTGGCAGGTTGGGGCCAGACCAATGCTGCTGACAAAAACTCTGTGAAAACGGATCTGATGAAA
GTGCCAATGGTCATCATGGACTGGGAGGAGTGTTCAAAGATGTTTCCAAAACTTACCAAAAATATGCTGTGTGCCGGATA
CAAGAATGAGAGCTATGATGCCTGCAAGGGTGACAGTGGGGGGCCTCTGGTCTGCACCCCAGAGCCTGGTGAGAAGTGGT
ACCAGGTGGGCATCATCAGCTGGGGAAAGAGCTGTGGAGAGAAGAACACCCCAGGGATATACACCTCGTTGGTGAACTAC
AACCTCTGGATCGAGAAAGTGACCCAGCTAGAGGGCAGGCCCTTCAATGCAGAGAAAAGGAGGACTTCTGTCAAACAGAA
ACCTATGGGCTCCCCAGTCTCGGGAGTCCCAGAGCCAGGCAGCCCCAGATCCTGGCTCCTGCTCTGTCCCCTGTCCCATG
TGTTGTTCAGAGCTATTTTGTAC**TGA**TAATAAAATAGAGGCTATTCTTTCAACCGAAA

The FCTR6b protein encoded by SEQ ID NO:22 has 267 amino acid residues and is presented using the one-letter code in Table 6B. The Psort profile for FCTR4 predicts that this sequence has no N-terminal signal peptide and is likely to be localized at the mitochondrial matrix space (Certainty=0.4372). The predicted molecular weight of this protein is 29498.9 Daltons.

Table 6D. Encoded FCTR6b protein sequence (SEQ ID NO:23).

```
MGFRFLGTANSATFETSLPLPLAPLWFSATSPEELSVVLGTNDLTSPSMEIKEVASIILHKDFKRANMDNDIALLLLASPIKLDDL
KVPICLPTQPGPATWRECWVAGWGQTNAADKNSVKTDLMKVPMVIMDWEECSKMFPKLTKNMLCAGYKNESYDACKGDSGGPLVCT
PEPGEKWYQVGIISWGKSCGEKNTPGIYTSLVNYNLWIEKVTQLEGRPFNAEKRRTSVKQKPMGSPVSGVPEPGSPRSWLLLCPLS
HVLFRAILY
```

In a search of sequence databases, it was found, for example, that the FCTR6a nucleic acid sequence has 853 of 897 bases (95 %) identical to bases 551-1447, and 346 of 388 bases (89%) identical to bases 127-513 of *Macaca fascicularis* brain cDNA, clone QccE-17034 (GENBANK-ID: |AB046651) (Table 6E).

Table 6E. BLASTN of FCTR6a against *Macaca fascicularis* brain cDNA, clone QccE-17034 (SEQ ID NO:82)

```
>GI|9651112|DBJ|AB046651.1|AB046651 MACACA FASCICULARIS BRAIN CDNA, CLONE QCCE-17034
          LENGTH = 1746

 SCORE = 1429 BITS (721), EXPECT = 0.0
 IDENTITIES = 853/897 (95%)
 STRAND = PLUS / PLUS

QUERY: 434   CCTTTTTCCAATCCTCACACCTTCTGATCAACAGCCCCAGTAGGGTTTAAAGGTCCTAGA 493
             ||||||||||||||||||||||||||| | |||||||||||||||| |||| ||||||||
SBJCT: 551   CCTTTTTCCAATCCTCACACCTTCTGAGCTACAGCCCCAGTAGGGTCTAAATGTCCTAGA 610

QUERY: 494   GCTACATGGGATTTAGGTTTCTGGGCACAGCCAATTCTGCCACTTTTGAGACTTCCCTTC 553
             |||| ||| |||||||||||||| |||||||||||||| ||||||||||| |||||||||
SBJCT: 611   GCTATATGAGATTTAGGTTTCTGAGCACAGCCAATTCTCCCACTTTTGAGGCTTCCCTTC 670

QUERY: 554   CCCTTCCACTTGCCCCTCTCTGGTTCTCTGCCACCAGTCCAGAAGAACTGAGTGTCGTGC 613
             ||||| |||| |||||||||||||||||||||||||||||||||||||||| ||||||||
```

```
SBJCT: 671   CCCTTTCACTCGCCCCTCTCTGGTTCTCTGCCACCAGTCCAGAAGAACTGAATGTCGTGC 730

QUERY: 614   TGGGGACCAACGACTTAACTAGCCCATCCATGGAAATAAAGGAGGTCGCCAGCATCATTC 673
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
SBJCT: 731   TGGGGACCAACGACTTAACTAGCTCATCCATGGAAATAAAGGAGGTCGCCAGCATCATTC 790

QUERY: 674   TTCACAAAGACTTTAAGAGAGCCAACATGGACAATGACATTGCCTTGCTGCTGCTGGCTT 733
             ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||| |
SBJCT: 791   TTCACAAGGACTTTAAGAGAGCCAACATGGACAATGACATTGCCTTGCTGCTGCTGGCCT 850

QUERY: 734   CGCCCATCAAGCTCGATGACCTGAAGGTGCCCATCTGCCTCCCCACGCAGCCCGGCCCTG 793
             |||||||||  |||||||||||||||||||||||||||||||| ||||||| |||||| |
SBJCT: 851   CGCCCATCACACTCGATGACCTGAAGGTGCCCATCTGCCTCCCTACGCAGCACGGCCCCG 910

QUERY: 794   CCACATGGCGCGAATGCTGGGTGGCAGGTTGGGGCCAGACCAATGCTGCTGACAAAAACT 853
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 911   CCACATGGCACGAATGCTGGGTGGCAGGTTGGGGCCAGACCAATGCTGCTGACAAAAACT 970

QUERY: 854   CTGTGAAAACGGATCTGATGAAAGTGCCAATGGTCATCATGGACTGGAGGAGTGTTCAA 913
             |||||||||||||||||||||||| ||| |||||||||||||||||||||||||||||||
SBJCT: 971   CTGTGAAAACGGATCTGATGAAAGCGCCGATGGTCATCATGGACTGGAGGAGTGTTCAA 1030

QUERY: 914   AGATGTTTCCAAAACTTACCAAAAATATGCTGTGTGCCGGATACAAGAATGAGAGCTATG 973
             ||  |||||||||||| |||||||||||||||||||| |||||||| |||||||||||||
SBJCT: 1031  AGGCGTTTCCAAAACTCACCAAAAATATGCTGTGTGCTGGATACAATAATGAGAGCTATG 1090

QUERY: 974   ATGCCTGCAAGGGTGACAGTGGGGGGCCTCTGGTCTGCACCCCAGAGCCTGGTGAGAAGT 1033
             | |||||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||
SBJCT: 1091  ACGCCTGCCAGGGTGACAGCGGGGGACCTCTGGTCTGCACCCCAGAGCCTGGTGAGAAGT 1150

QUERY: 1034  GGTACCAGGTGGGCATCATCAGCTGGGGAAAGAGCTGTGGAGAGAAGAACACCCCAGGGA 1093
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
SBJCT: 1151  GGTACCAGGTGGGTATCATCAGCTGGGGAAAGAGCTGTGGAGAGAAGAACACCCCAGGGA 1210

QUERY: 1094  TATACACCTCGTTGGTGAACTACAACCTCTGGATCGAGAAAGTGACCCAGCTAGAGGGCA 1153
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
SBJCT: 1211  TATACACCTCGTTGGTGAACTACAACCTCTGGATCGAGAAGGTGACCCAGCTAGAGGGCA 1270
QUERY: 1154  GGCCCTTCAATGCAGAGAAAAGGAGGACTTCTGTCAAACAGAAACCTATGGGCTCCCCAG 1213
             ||||||||| ||| ||||||| |||||| |||||||||||||||||||||||||||| ||
SBJCT: 1271  GGCCCTTCAGTGCGGAGAAAATGAGGACCTCTGTCAAACAGAAACCTATGGGCTCCCGAG 1330

QUERY: 1214  TCTCGGGAGTCCCAGAGCCAGGCAGCCCCAGATCCTGGCTCCTGCTCTGTCCCCTGTCCC 1273
             ||||||| ||||||||||||||| ||| ||||||||||||||||||||||||||||||||
SBJCT: 1331  TCTCGGGGGTCCCAGAGCCAGGCGGCCTCAGATCCTGGCTCCTGCTCTGTCCCCTGTCCC 1390

QUERY: 1274  ATGTGTTGTTCAGAGCTATTTTGTACTGATAATAAAATAGAGGCTATTCTTTCAACC 1330
             |||||||||||||||||||||||||||||||||||||||||||||||| ||| ||||
SBJCT: 1391  ATGTGTTGTTCAGAGCTATTTTGTACTGATAATAAAATAGAGGCTATTTTTTTAACC 1447

 SCORE =  428 BITS (216), EXPECT = E-117
 IDENTITIES = 346/388 (89%), GAPS = 1/388 (0%)
 STRAND = PLUS / PLUS

QUERY: 1     GATTTTAGAAGGTTAATCAAAAACCCGGGGACAGTTTCTTCATGGCATAACCACAGACCT 60
             ||||||||||||||||||||||||||  |||||||||| ||||| |||||||| |||||
SBJCT: 127   GATTTTAGAAGGTTAATCAAAAACCCAAGGACAGTTTCATCATGTCATAACCAAAGACCC 186

QUERY: 61    TTGTGGCACCCGCTGTCGTGGGATATCAAATATCCTCTGGGGTTCGGAATGTGGGCTTAT 120
             |||||||||| |||||| ||||||| |||||||| | |||||||| |||||||| |||||
SBJCT: 187   TTGTGGCACCTGCTGTCATGGGATAACAAATATCTTGTGGGGTTCTGAATGTGGACTTAT 246

QUERY: 121   TACTGAAGATCCTGTCTGCTTGGTCAGTGGCAGGTCTAGACTAACTTCTGGTCCTGAGTT 180
             |||||||| |||||||||||||||||||||  |||||||||||||||||||||||||| |
SBJCT: 247   TACTGAAGCTCCTGTCTGCTTGGTCAGTGG-TGGTCTAGACTAACTTCTGGTCCTGAGAT 305

QUERY: 181   TCTAAAGTGCTGGTAGACCAGTTGATACAAAACAGATATAATAATGAATGCCTTATCTAT 240
             ||||||||| ||||||||| ||||| | |||| | |||||||||||||||||||| ||||
SBJCT: 306   TCTAAAGTGTTGGTAGACCGGTTGAGATAAAAGATATATAATAATGAATGCCTTACCTAT 365

QUERY: 241   CTGAAGGTCAGTTTGATCCGTGCCAAGTGGCTTTTTGTGGCTGTGTAGAGTGCTCTAAA 300
```

```
                |||||  ||||||||||||||||||| ||||||||||||||| |||||||||| |||||
SBJCT: 366  CTGAAAACCAGTTTGATCCGTGCCAAGGGGCTTTTGTGGGCTCTGTAGAGTGCCCTAAA 425

QUERY: 301  CCCAGCTCGGCCTTTGCTGTATTAGACAGAAGCACCTCATTCATATCCCTGGGGCCCCTG 360
            |||||||| ||||||||||| ||||||||||||||  |||||| ||| ||||||||||
SBJCT: 426  CCCAGCTCTGCCTTTGCTGTGTTAGACAGAAGCACGCCATTCACATCTCTGGGGCCCCCA 485

QUERY: 361  ATGGTGCAGTGGTCTGGCTGTGGTCTGC 388
            |||||||  |||| ||| ||||||||||
SBJCT: 486  ATGGTGCCATGGTGTGGTTGTGGTCTGC 513
```

In a search of sequence databases, it was found, for example, that the FCTR6a nucleic acid sequence has 295 of 378 bases (78 %) identical to bases 410-779 of *Mus musculus* adult male testis cDNA, RIKEN full-length enriched (GENBANK-ID:AK09660) (Table 6F).

Table 6F. BLASTN of FCTR6a against *Mus musculus* adult male testis cDNA, RIKEN full-length enriched (SEQ ID NO:83)

```
>GI|12855429|DBJ|AK016601.1|AK016601 MUS MUSCULUS ADULT MALE TESTIS CDNA, RIKEN FULL-
LENGTH ENRICHED
            LIBRARY, CLONE:4933401F05, FULL INSERT SEQUENCE
          LENGTH = 1047

 SCORE = 97.6 BITS (49), EXPECT = 2E-17
 IDENTITIES = 295/378 (78%), GAPS = 8/378 (2%)
 STRAND = PLUS / PLUS

QUERY: 697   AACATGGACAATGACATTGCCTTGCTGCTGCTGGCTTCGCCCATCAAGCTCGATGACCTG 756
             ||||||||||| |||||||||||| ||||||| ||   |||| | | | || |||| |||
SBJCT: 410   AACATGGACAACGACATTGCCTTGTTGCTGCTAGCCAAGCCCTTGACGTTCAATGAGCTG 469

QUERY: 757   AAGGTGCCCATCTGCCTCCCCACGCAGCCCGGCCCTGCCACATGGCGCGAATGCTGGGTG 816
             | ||||||||||||||| ||      ||||| |||| |||  |||| |||||||||||||
SBJCT: 470   ACGGTGCCCATCTGCCTTCCTCTCTGGCCCGCCCCTCCCAGCTGGCACGAATGCTGGGTG 529

QUERY: 817   GCAGGTTGGGGCCAGACCAATGCTGCTGACAAAAACTCTGTGAAAACGGATCTGATGAAA 876
             ||||| ||||||   |||||  |  |||||||  | ||| ||  |||||||||||||||
SBJCT: 530   GCAGGATGGGGCGTAACCAACTCAACTGACAAGGAATCTATGTCAACGGATCTGATGAAG 589

QUERY: 877   GTGCCAATGGTCATCATGGACTGGGAGGAGTGTTCAAAGATGTTTCCAAAACTTACCAAA 936
             ||||| |||   ||||| || |||||||| || | | |||||||||| |  || |||| |
SBJCT: 590   GTGCCCATGCGTATCATAGAGTGGGAGGAATGCTTACAGATGTTTCCCAGCCTCACCACA 649

QUERY: 937   AATATGCTGTGTGCCGGATACAAGAATGAGAGCTATGATGCCTGCAAGGGTGACAGTGGG 996
             || ||||||||||||  |||    ||||||||||| ||||| |||        |||||||
SBJCT: 650   AACATGCTGTGTGCCTCATATGGTAATGAGAGCTACGATGCTTGC--------CAGTGGG 701

QUERY: 997   GGGCCTCTGGTCTGCACCCCAGAGCCTGGTGAGAAGTGGTACCAGGTGGGCATCATCAGC 1056
             || || || ||||||||| |||| |||||    | |||||||||||||||||||||||||
SBJCT: 702   GGACCGCTTGTCTGCACCACAGATCCTGGCAGTAGGTGGTACCAGGTGGGCATCATCAGC 761

QUERY: 1057  TGGGGAAAGAGCTGTGGA 1074
             ||||| ||||||||||||
SBJCT: 762   TGGGGCAAGAGCTGTGGA 779
```

The FCTR6a amino acid has 247 of 267 amino acid residues (92%) identical to, and 251 of 307 residues (94%) positive with, the 267 amino acid hypothetical protein [*Macaca fascicularis*] (GenBank: AB046651) (SEQ ID NO:84) (Table 6G).

Table 6G. BLASTP of FCTR6a and b against hypothetical protein [*Macaca fascicularis*] (SEQ ID NO:84)

```
>GI|9651113|DBJ|BAB03569.1| (AB046651) HYPOTHETICAL PROTEIN [MACACA FASCICULARIS]
          LENGTH = 267

 SCORE =  467 BITS (1202), EXPECT = E-131
 IDENTITIES = 247/267 (92%), POSITIVES = 251/267 (94%)

QUERY: 1    MGFRFLGTANSATFETSLPLPLAPLWFSATSPEELSVVLGTNDLTSPSMEIKEVASIILH 60
            | |||| |||| ||| |||| |||||||||||||+||||||||| ||||||||||||
SBJCT: 1    MRFRFLSTANSPTFEASLPLSLAPLWFSATSPEELNVVLGTNDLTSSSMEIKEVASIILH 60

QUERY: 61   KDFKRANMDNDIALLLLASPIKLDDLKVPICLPTQPGPATWRECWVAGWGQTNAADKNSV 120
            |||||||||||||||||||| ||||||||||||| ||||| |||||||||||||||||
SBJCT: 61   KDFKRANMDNDIALLLLASPITLDDLKVPICLPTQHGPATWHECWVAGWGQTNAADKNSV 120

QUERY: 121  KTDLMKVPMVIMDWEECSKMFPKLTKNMLCAGYKNESYDACKGDSGGPLVCTPEPGEKWY 180
            |||||| |||||||||||| |||||||||||| |||||||+||||||||||||||||
SBJCT: 121  KTDLMKAPMVIMDWEECSKAFPKLTKNMLCAGYNNESYDACQGDSGGPLVCTPEPGEKWY 180
                              K                        E
QUERY: 181  QVGIISWGKSCGDKNTPGIYTSLVNYNLWIEKVTQLGGRPFNAEKRRTSVKQKPMGSPVS 240
            |||||||||||+|||||||||||||||||||||||| ||||+||| ||||||||||| ||
SBJCT: 181  QVGIISWGKSCGEKNTPGIYTSLVNYNLWIEKVTQLEGRPFSAEKMRTSVKQKPMGSRVS 240

QUERY: 241  GVPEPGSPRSWLLLCPLSHVLFRAILY 267
            ||||||| ||||||||||||||||||
SBJCT: 241  GVPEPGGLRSWLLLCPLSHVLFRAILY 267

K AND E ARE RESIDUES THAT DIFFER BETWEEN FCTR6A AND B. D193K, AND G217E.
```

The FCTR6a amino acid has 80 of 201 amino acid residues (39%) identical to, and 119 of 201 residues (58%) positive with, the 638 amino acid plasma kallikrein B1 precursor (GENBANK-ID:NP_000883.1) (SEQ ID NO:85) (Table 6H).

Table 6H. BLASTP of FCTR6a and b against plasma kallikrein B1 precursor (SEQ ID NO:85)

```
>GI|4504877|REF|NP_000883.1| PLASMA KALLIKREIN B1 PRECURSOR; KALLIKREIN, PLASMA;
KALLIKREIN B
            PLASMA; KALLIKREIN 3, PLASMA; FLETCHER FACTOR [HOMO
            SAPIENS]
 GI|125184|SP|P03952|KAL_HUMAN PLASMA KALLIKREIN PRECURSOR (PLASMA PREKALLIKREIN)
(KININOGENIN)
            (FLETCHER FACTOR)
 GI|67591|PIR||KQHUP PLASMA KALLIKREIN (EC 3.4.21.34) PRECURSOR - HUMAN
 GI|190263|GB|AAA60153.1| (M13143) PLASMA PREKALLIKREIN [HOMO SAPIENS]
 GI|8809781|GB|AAF79940.1| (AF232742) PLASMA KALLIKREIN PRECURSOR [HOMO SAPIENS]
          LENGTH = 638

 SCORE =  133 BITS (334), EXPECT = 3E-30
 IDENTITIES = 80/201 (39%), POSITIVES = 119/201 (58%), GAPS = 18/201 (8%)

QUERY: 20   LPLAPLWFSATSPEELSVVLGTNDLT--SPSMEIKEVASIILHKDFKRANMDNDIALLLL 77
            |||   +|          | +|   +|+|   +|   +|||   ||+|+++| +   ++||||+ |
SBJCT: 439  LPLQDVW------RIYSGILNLSDITKDTPFSQIKE---IIIHQNYKVSEGNHDIALIKL 489

QUERY: 78   ASPIKLDDLKVPICLPTQPGPAT-WRECWVAGWGQTNAADKNSVKTDLMKVPMVIMDWEE 136
             +|+    + +  |||||++    +| +    ||| ||| +    +|  ++   | || + ++  ||
SBJCT: 490  QAPLNYTEFQKPICLPSKGDTSTIYTNCWVTGWGFSK--EKGEIQNILQKVNIPLVTNEE 547
                                                                       K
QUERY: 137  CSKMFP--KLTKNMLCAGYKNESYDACKGDSGGPLVCTPEPGEKWYQVGIISWGKSCGDK 194
```

```
                 | |  +    |+|+ |+|||||    |||||||||||||   +     |   ||| |||+ |   +
SBJCT: 548 CQKRYQDYKITQRMVCAGYKEGGKDACKGDSGGPLVC--KHNGMWRLVGITSWGEGCARR 605

QUERY: 195 NTPGIYTSLVNYNLWIEKVTQ 215
            ||+|| +  |  || + ||
SBJCT: 606 EQPGVYTKVAEYMDWILEKTQ 626

K IS A RESIDUE THAT DIFFERS BETWEEN FCTR6A AND B. D193K.
```

The FCTR6a amino acid has 73 of 183 amino acid residues (39%) identical to, and 110 of 183 residues (59%) positive with, the 643 amino acid kallikrein [*Sus scrofa*] (GENBANK-ID:BAA37147.1) (SEQ ID NO:86) (Table 6I).

Table 6I. BLASTP of FCTR6a and b against kallikrein [*Sus scrofa*] (SEQ ID NO:86)

```
>GI|4165315|DBJ|BAA37147.1| (AB022425) KALLIKREIN [SUS SCROFA]
          LENGTH = 643

 SCORE =  128 BITS (322), EXPECT = 9E-29
 IDENTITIES = 73/183 (39%), POSITIVES = 110/183 (59%), GAPS = 12/183 (6%)

QUERY: 38  VLGTNDLT--SPSMEIKEVASIILHKDFKRANMDNDIALLLLASPIKLDDLKVPICLPTQ 95
           +|  +++|  +|  ++||  ||+|+++|      +||||| | +|+    | + |||||++
SBJCT: 459 ILNISEITKETPFSQVKE---IIIHQNYKILESGHDIALLKLETPLNYTDFQKPICLPSR 515

QUERY: 96  PGP-ATWRECWVAGWGQTNAADKNSVKTDLMKVPMVIMDWEECSKMFP--KLTKNMLCAG 152
                  + ||| ||| |   +|  ++  | || + ++  ||| | +    |++| |+|||
SBJCT: 516 DDTNVVYTNCWVTGWGFTE--EKGEIQNILQKVNIPLVSNEECQKSYRDHKISKQMICAG 573
                                                         K
QUERY: 153 YKNESYDACKGDSGGPLVCTPEPGEKWYQVGIISWGKSCGDKNTPGIYTSLVNYNLWIEK 212
           ||     |||||+|||||||  +     |+ ||  |||+ |   +   ||+|| ++ |   || +
SBJCT: 574 YKEGGKDACKGESGGPLVC--KYNGIWHLVGTTSWGEGCARREQPGVYTKVIEYMDWILE 631

QUERY: 213 VTQ 215
            ||
SBJCT: 632 KTQ 634

K IS A RESIDUE THAT DIFFERS BETWEEN FCTR6A AND B. D193K.
```

The FCTR6a amino acid has 81 of 205 amino acid residues (39%) identical to, and 112 of 205 residues (54%) positive with, the 625 amino acid Coagulation factor XI [*Homo sapiens*] (embCAA64368.1) (SEQ ID NO:87) (Table 6J).

Table 6J. BLASTP of FCTR6a and b against Coagulation factor XI [*Homo sapiens*] (SEQ ID NO:87)

```
>GI|180352|GB|AAA51985.1| (M20218) COAGULATION FACTOR XI [HOMO SAPIENS]
          LENGTH = 625

 SCORE =  127 BITS (320), EXPECT = 1E-28
 IDENTITIES = 81/205 (39%), POSITIVES = 112/205 (54%), GAPS = 17/205 (8%)

QUERY: 20  LPLAPLWFSATSPEELSVVLGTNDLTSPSMEIKE------VASIILHKDFKRANMDNDIA 73
           |  |  ++   ||+ | |  |  + +    ||||       |  ||+|  +| |    |||
SBJCT: 427 LTAAHCFYGVESPKILRVYSGILNQS----EIKEDTSFFGVQEIIIHDQYKMAESGYDIA 482

QUERY: 74  LLLLASPIKLDDLKVPICLPTQPG-PATWRECWVAGWGQTNAADKNSVKTDLMKVPMVIM 132
           || | + +   | + |||||++       + +||| |||        ||  ++  | |  + ++
SBJCT: 483 LLKLETTVNYTDSQRPICLPSKGDRNVIYTDCWVTGWGYRKLRDK--IQNTLQKAKIPLV 540

QUERY: 133 DWEECSKMFP--KLTKNMLCAGYKNESYDACKGDSGGPLVCTPEPGEKWYQVGIISWGKS 190
```

```
           ||| | +   |+|  |+||||+    ||||||||||| |   +  | |+ ||| |||+
SBJCT: 541 TNEECQKRYRGHKITHKMICAGYREGGKDACKGDSGGPLSC--KHNEVWHLVGITSWGEG 598
             K
QUERY: 191 CGDKNTPGIYTSLVNYNLWIEKVTQ 215
           |  +  ||+||++|  |   || + ||
SBJCT: 599 CAQRERPGVYTNVVEYVDWILEKTQ 623

K IS A RESIDUE THAT DIFFERS BETWEEN FCTR6A AND B. D193K.
```

The number of new cases of renal cell carcinoma in the United States in 1996 was projected to be 30,600 with an estimated 12,000 deaths. Tumors with a proposed histogenesis from the proximal tubule (clear-cell and chromophilic tumors) amount to 85% of renal cancers, whereas tumors with a proposed histogenesis from the connecting tubule/collecting duct (chromophobic-, oncocytic-, and duct Bellini-type tumors) amount to only 11%.

Adenocarcinomas may be separated into clear cell and granular cell carcinomas, although the 2 cell types may occur together in some tumors. The distinction between well-differentiated renal carcinomas and renal adenomas can be difficult. The diagnosis is usually made arbitrarily on the basis of size of the mass, but size alone should not influence the treatment approach, since metastases can occur with lesions as small as 0.5 centimeters.

While radical nephrectomy with regional lymphadenectomy, is the accepted, often curative therapy for stage I (localized disease) renal cell cancer, very little therapy is available for advance disease that represent about 70% of the patients. Radiotherapy as a postoperative adjuvant has not been effective, and when used preoperatively, may decrease local recurrence but does not appear to improve 5-yr survival. A chemotherapeutic agent capable of significantly altering the course of metastastic renal cell carcinoma has not been identified. (Renal Cell Cancer (PDQ®) Treatment - Health Professionals, Cancernet, NCI)

There is therefore a need to identify genes that are differentially modulated in renal-cell carcinomas. In addition there is a need for methods to assay candidate therapeutic substances for modulating expression of these genes. These substances might be recombinant protein expressed by the identified genes or antibodies that bind to the identified proteins. There is yet additionally a need for an effective method of identifying target molecules or related components. These and related needs and defects are addressed in the present invention.

Novel kallikrein-like/coagulation factor XI-like Proteins and Nucleic Acids Encoding Same

FCTR6 is surprisingly found to be differentially expressed in clear cell Renal cell carcinoma tissues vs the normal adjacent kidney tissues. The present invention discloses a novel protein encoded by a cDNA and/or by genomic DNA and proteins similar to it, namely, new proteins bearing sequence similarity to kallikrein-like, nucleic acids that encode these proteins or

fragments thereof, and antibodies that bind immunospecifically to a protein of the invention. It may have use as a therapeutic agent in the treatmentof renal cancer and liver cirrhosis.

The utility of kallikrein family members in protein therapy of Renal cancer

The treatment of renal cell carcinoma with recombinant kallikrein could improve disease outcome through several potential mechanisms. The literature suggests that members of this protein family are inhibitory to the process of angiogenesis, a process of vital importance to tumor progression. Renal cell carcinoma is known to be a highly angiogenic cancer. Thus, treatment of renal cell carcinoma with kallikrein may effectively shutdown the active recruitment of a blood supply to a tumor. Members of this protein family are known to play a role in vascular coagulation. Similar to anti-angiogenic therapy, a factor produced by cancer cells that is pro-coagulatory may also act to inhibit cancer growth by effectively "clogging" the tumor vascular supply. In addition, through its proteolytic activity, kallikrein may degrade ECM proteins or growth factors necessary for the progressive growth of cancer cells. Following is a relevant reference underlining the importance of Kallikrein in cancer therapy.

The New Human Kallikrein Gene Family: Implications in Carcinogenesis.

Diamandis EP; Yousef GM; Luo I; Magklara I; Obiezu CV

Department of Pathology and Laboratory Medicine, Mount Sinai Hospital, Toronto, Ontario, Canada.

Trends Endocrinol Metab 2000 Mar;11(2):54-60.

ABSTRACT: The traditional human kallikrein gene family consists of three genes, namely KLK1 [encoding human kallikrein 1 (hK1) or pancreatic/renal kallikrein], KLK2 (encoding hK2, previously known as human glandular kallikrein 1) and KLK3 [encoding hK3 or prostate-specific antigen (PSA)]. KLK2 and KLK3 have important applications in prostate cancer diagnostics and, more recently, in breast cancer diagnostics. During

the past two to three years, new putative members of the human kallikrein gene family have been identified, including the PRSSL1 gene [encoding normal epithelial cell-specific 1 gene (NES1)], the gene encoding zyme/protease M/neurosin, the gene encoding prostase/KLK-L1, and the genes encoding neuropsin, stratum corneum chymotryptic enzyme and trypsin-like serine protease. Another five putative kallikrein genes, provisionally named KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-L6, have also been identified. Many of the newly identified kallikrein-like genes are regulated by steroid hormones, and a few kallikreins (NES1, protease M, PSA) are known to be downregulated in breast and possibly other cancers. NES1 appears to

be a novel breast cancer tumor suppressor protein and PSA a potent inhibitor of angiogenesis. This brief review summarizes recent developments and possible applications of the newly defined and expanded human kallikrein gene locus.

The utility of kallikrein-like/coagulation factor XI-like family members in protein therapy of liver cirrosis

Results related to inflammation shown below in Example A, Table CC3, panel 4, indicate over-expression of 27455183.0.19 in the liver cirrhosis sample, as compared to panel 1 data (Table CC1), where there is little or no expression in normal adult liver. Panel 4 was generated from various human cell lines that were untreated or resting as well as the same cells that were treated with a wide variety of immune modulatory molecules. There are several disease tissues represented as well as organ controls.

Potential Role(s) of FCTR6 in Inflammation:

Liver cirrhosis occurs in patients with hepatitis C and also in alcoholics. This protein is 41% related to coagulation factor XI and its potential role in liver cirrhosis may be related to cleavage of kininogen. A reference for this follows:

Thromb Haemost 2000 May;83(5):709-14 High molecular weight kininogen is cleaved by FXIa at three sites: Arg409-Arg410, Lys502-Thr503 and Lys325-Lys326. Mauron T, Lammle B, Wuillemin WA Central Hematology Laboratory, University of Bern, Inselspital, Switzerland. Abstract:

We investigated the cleavage of high molecular weight kininogen (HK) by activated coagulation factor XI (FXIa) in vitro. Incubation of HK with FXIa resulted in the generation of cleavage products which were subjected to SDS-Page and analyzed by silverstaining, ligand-blotting and immunoblotting, respectively. Upon incubation with FXIa, bands were generated at 111, 100, 88 kDa on nonreduced and at 76, 62 and 51 kDa on reduced gels. Amino acid sequence analysis of the reaction mixtures revealed three cleavage sites at Arg409-Arg410, at Lys502-Thr503 and at Lys325-Lys326. Analysis of HK-samples incubated with FXIa for 3 min, 10 min and 120 min indicated HK to be cleaved first at Arg409-Arg410, followed by cleavage at Lys502-Thr503 and then at Lys325-Lys326. In conclusion, HK is cleaved by FXIa at three sites. Cleavage of HK by FXIa results in the loss of the surface binding site of HK, which may constitute a mechanism of inactivation of HK and of control of contact system activation.

Impact of Therapeutic Targeting of FCTR6 in Inflammation:

Therapeutic targeting of FCTR6 with a monoclonal antibody is anticipated to limit or block the extent of breakdown of kininogen and thereby reduce the degradation of liver that occurs in liver cirrhosis. A pertinent reference is:

Thromb Haemost 1999 Nov;82(5):1428-32 Parallel reduction of plasma levels of high and low molecular weight kininogen in patients with cirrhosis.

Cugno M, Scott CF, Salerno F, Lorenzano E, Muller-Esterl W, Agostoni A, Colman RW
Department of Internal Medicine, IRCCS Maggiore Hospital, University of Milan, Italy.
massimo.cugno@unimi.it

Abstract:

Little is known about the regulation of high-molecular-weight-kininogen (HK) and low-molecular-weight-kininogen (LK) or the relationship of each to the degree of liver function impairment in patients with cirrhosis. In this study, we evaluated HK and LK quantitatively by a recently described particle concentration fluorescence immunoassay (PCFIA) and qualitatively by SDS PAGE and immunoblotting analyses in plasma from 33 patients with cirrhosis presenting various degrees of impairment of liver function. Thirty-three healthy subjects served as normal controls. Patients with cirrhosis had significantly lower plasma levels of HK (median 49 microg/ml [range 22-99 microg/ml]) and LK (58 microg/ml [15-100 microg/ml]) than normal subjects (HK 83 microg/ml [65-115 microg/ml]; LK 80 microg/ml [45-120 microg/ml]) ($p<0.0001$). The plasma concentrations of HK and LK were directly related to plasma levels of cholinesterase ($P<0.0001$) and albumin ($P<0.0001$ and $P<0.001$) and inversely to the Child-Pugh score ($P<0.0001$) and to prothrombin time ratio ($P<0.0001$) (reflecting the clinical and laboratory abnormalities in liver disease). Similar to normal individuals, in patients with cirrhosis, plasma HK and LK levels paralleled one another, suggesting that a coordinate regulation of those proteins persists in liver disease. SDS PAGE and immunoblotting analyses of kininogens in cirrhotic plasma showed a pattern similar to that observed in normal controls for LK (a single band at 66 kDa) with some lower molecular weight forms noted in cirrhotic plasma. A slight increase of cleavage of HK (a major band at 130 kDa and a faint but increased band at 107 kDa) was evident. The increased cleavage of HK was confirmed by the lower cleaved kininogen index (CKI), as compared to normal controls. These data suggest a defect in hepatic synthesis as well as increased destructive cleavage of both kininogens in plasma from patients with cirrhosis. The decrease of important regulatory proteins like kininogens may contribute to the imbalance in coagulation and fibrinolytic systems, which frequently occurs in cirrhotic patients.

In summary, the differential expression of FCTR6 (Kallikrein family) in renal cell carcinoma is an important finding that could have immense potential in renal carcinogenesis. In

additon, overexpression of the above gene in liver cirrhosis demonstrates its anticipated use as an immunotherapeutic target.

FCTR7

The novel nucleic acid of 1498 nucleotides FCTR7 (also designated. 32592466.0.64) encoding a novel trypsin inhibitor-like protein is shown in Table 7A. An ORF begins with an ATG initiation codon at nucleotides 470-472 and ends with a TAA codon at nucleotides 1369-1371. Putative untranslated regions, if any, are found upstream from the initiation codon and downstream from the termination codon.

Table 7A. FCTR7 Nucleotide Sequence (SEQ ID NO:24)

AGGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCCGCCGAGCCTCGTTCGTGTCC
CCGCCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCCACCCTGGCAGACTAACGAAGCAGCTCCCTTCCCACCCCAA
CTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGCCGCAGAGGCGGAGGCTCGCGTATTCCTGCAGT
CAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTCGCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGG
GCGGCTGCAGAGGCCGGCCGTCCGGTTTGGCTCACCTCTCCCAGGAAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGT
CTTGGAGATTTTCCTGGGGAAATCCTGAGGTCATTCATT**ATG**AAGTGTACCGCGCGGGAGTGGCTCAGAGTAACCACAGTGCTGTT
CATGGCTAGAGCAATTCCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAAACTTTTGGAAAAATACATGGATGAGGATGGTG
AGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCATAATAAATTACGA
AGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGATCTGCAGAATCCAGGGCTGAAAT
TGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAATTTGGAGCACACTGGGGAAGATATAGGCCCCCGAC
GTTTCATGTACAATCGTGGTATGATGAAGTGAAAGACTTTAGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTCAGGT
GTTCTGGCCCTGTATGTACACATTATACACAGGTCGTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTCATAAC
ATGAACATCTGGGGGCAGATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAAACTGGTGGGGCCATGCCCC
TTACAAACATGGGCGGCCCTGTTCTGCTTGCCCACCTAGTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGGTCAG
ACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGGCAGCAGTCACAAGTCCATGACACCCATGTCCGGACAAGA
TCAGATGATAGTAGCAGAAATGAAGTCATTAGCTTTGGGAAAAGTAATGAAAATATAATGGTTTTAGAAATCCTGTGT**TAA**ATATT
GCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATTGTTCTACGTTTCATATATTATATGGTGCTTTGTATA
TGCCCCTAATAAAATGAATCTAAACATTGAAAAAAA

The FCTR7 protein encoded by SEQ ID NO:24 has 300 amino acid residues and is presented using the one-letter code in Table 7B. The FCTR7 gene was found to be expressed in: brain; germ cell tumors. FCTR7 gene maps to Unigene cluster Hs.182364 which is expressed in the following tissues: brain, breast, ear, germ cell, heart, liver, lung, whole embryo, ovary, pancreas, pooled, prostate, stomach, testis, uterus, vascular. Therefore the FCTR7 protein described in this invention is also expressed in the above tissues.

The SignalP, Psort and/or Hydropathy profile for FCTR7 predict that this sequence has a signal peptide and is likely to be localized outside of the cell with a certainty of 0.4228. The SignalP shows a cleavage site between amino acids 20 and 21, *i.e.*, at the dash in the sequence amino acid ARA-IP. The predicted molecular weight of FCTR7 is 34739.9 Daltons. Hydropathy profile shows an amino terminal hydrophobic region. This region could function as a signal peptide and target the invention to be secreted or plasma membrane localized.

Table 7B. Encoded FCTR7 protein sequence (SEQ ID NO:25).

```
MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDMQSILDLHNKLRSQVYPTASNMEYM
TWDVELERSAESRAESCLWEHGPASLLPSIGQNLGAHWGRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVV
WATSNRIGCAINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYKEGSDRYYPPREEETNE
IERQQSQVHDTHVRTRSDDSSRNEVISFGKSNENIMVLEILC
```

This gene maps to Unigene cluster Hs.182364 which has been assigned the following mapping information shown in table 7C. Therefore the chromosomal assignment for this gene is the same as that for Unigene cluster 182364.

Table 7C. Mapping Information.

Chromosome:	8
Gene Map 98:	Marker SHGC-32056 , Interval D8S279-D8S526
Gene Map 98:	Marker SGC32056 , Interval D8S526-D8S275
Gene Map 98:	Marker sts-G20223 , Interval D8S526-D8S275
Gene Map 98:	Marker stSG30385 , Interval D8S526-D8S275
Whitehead map:	EST67946, Chr.8
dbSTS entries:	G25853, G29349, G20223

The predicted amino acid sequence was searched in the publicly available GenBank database

FCTR7 protein showed Score = 743 (261.5 bits), Expect = 1.4e-73, P = 1.4e-73, 54 % identities (129 over 237 amino acids) and 43% homologies (167 over 237 amino acids) with human 25 kD trypsin inhibitor protein (258 aa; ACC:O43692) (Table 7D).

Table 7D. BLAST X search results are shown below:

```
    ptnr:SPTREMBL-ACC:O43692 25 KDA TRYPSIN INHIBITOR - HO... +2 743 8.4e-73 1 (SEQ
ID NO:88)
    ptnr:SPTREMBL-ACC:O44228 HRTT-1 - HALOCYNTHIA RORETZI ... +2 325 2.9e-28 1 (SEQ
ID NO:89)
    ptnr:SWISSPROT-ACC:P48060 GLIOMA PATHOGENESIS-RELATED ... +2 314 5.3e-27 1 (SEQ
ID NO:90)
    ptnr:PIR-ID:JC4131 glioma pathogenesis-related protein... +2 309 2.0e-26 1 (SEQ
ID NO:91)
    ptnr:SWISSNEW-ACC:O19010 CYSTEINE-RICH SECRETORY PROTE... +2 258 9.4e-21 1 (SEQ
ID NO:92)
```

The nucleotide sequence of FCTR7 has 954 of 957 residues (99 %) identical to the 1-957 base segment, and 174 of 175 residues (99%) identical to bases 1317-1953 of the 2664

nucleotide *Homo sapiens* putative secretory protein precursor, mRNA (GenBank-ACC: AF142573) (SEQ ID NO:93) (Table 7E).

Table 7E. BLASTN of FCTR7 against Putative secretory protein precursor (SEQ ID NO:93)

```
>gi|12002310|gb|AF142573.1|AF142573 Homo sapiens putative secretory protein
precursor, mRNA, complete cds
          Length = 2664

 Score = 1865 bits (941), Expect = 0.0
 Identities = 954/957 (99%), Gaps = 1/957 (0%)
 Strand = Plus / Plus

Query: 364  gtccggtttggctcacctctcccaggaaacttcacactggagagccaaaaggagtggaag 423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    gtccggtttggctcacctctcccaggaaacttcacactggagagccaaaaggagtggaag 60

Query: 424  agcctgtcttggagattttcctggggaaatcctgaggtcattcattatgaagtgtaccgc 483
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   agcctgtcttggagattttcctggggaaatcctgaggtcattcattatgaagtgtaccgc 120

Query: 484  gcgggagtggctcagagtaaccacagtgctgttcatggctagagcaattccagccatggt 543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  gcgggagtggctcagagtaaccacagtgctgttcatggctagagcaattccagccatggt 180

Query: 544  ggttcccaatgccactttattggagaaacttttggaaaaatacatggatgaggatggtga 603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  ggttcccaatgccactttattggagaaacttttggaaaaatacatggatgaggatggtga 240

Query: 604  gtggtggatagccaaacaacgagggaaaagggccatcacagacaatgacatgcagagtat 663
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  gtggtggatagccaaacaacgagggaaaagggccatcacagacaatgacatgcagagtat 300

Query: 664  tttggaccttcataataaattacgaagtcaggtgtatccaacagcctctaatatggagta 723
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  tttggaccttcataataaattacgaagtcaggtgtatccaacagcctctaatatggagta 360

Query: 724  tatgacatgggatgtagagctggaaagatctgcagaatccagggctgaaa-ttgcttgtg 782
             |||||||||||||||||||||||||||||||||||||||| ||||||||| |||||||||
Sbjct: 361  tatgacatgggatgtagagctggaaagatctgcagaatcctgggctgaaagttgcttgtg 420

Query: 783  ggaacatggacctgcaagcttgcttccatcaattggacagaatttgggagcacactgggg 842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421  ggaacatggacctgcaagcttgcttccatcaattggacagaatttgggagcacactgggg 480

Query: 843  aagatataggcccccgacgtttcatgtacaatcgtggtatgatgaagtgaaagactttag 902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  aagatataggcccccgacgtttcatgtacaatcgtggtatgatgaagtgaaagactttag 540

Query: 903  ctacccatatgaacatgaatgcaacccatattgtccattcaggtgttctggccctgtatg 962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541  ctacccatatgaacatgaatgcaacccatattgtccattcaggtgttctggccctgtatg 600

Query: 963  tacacattatacacaggtcgtgtgggcaactagtaacagaatcggttgtgccattaattt 1022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601  tacacattatacacaggtcgtgtgggcaactagtaacagaatcggttgtgccattaattt 660

Query: 1023 gtgtcataacatgaacatctgggggcagatatggcccaaagctgtctacctggtgtgcaa 1082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661  gtgtcataacatgaacatctgggggcagatatggcccaaagctgtctacctggtgtgcaa 720
```

```
Query: 1083 ttactccccaaagggaaactggtggggccatgccccttacaaacatggcggccctgttc 1142
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721  ttactccccaaagggaaactggtggggccatgccccttacaaacatggcggccctgttc 780

Query: 1143 tgcttgcccacctagttttggagggggctgtagagaaaatctgtgctacaaagaagggtc 1202
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781  tgcttgcccacctagttttggagggggctgtagagaaaatctgtgctacaaagaagggtc 840

Query: 1203 agacaggtattatccccctcgagaagaggaaacaaatgaaatagaacggcagcagtcaca 1262
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct: 841  agacaggtattatccccctcgagaagaggaaacaaatgaaatagaacgacagcagtcaca 900

Query: 1263 agtccatgacacccatgtccggacaagatcagatgatagtagcagaaatgaagtcat 1319
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901  agtccatgacacccatgtccggacaagatcagatgatagtagcagaaatgaagtcat 957
```

```
Score =  339 bits (171), Expect = 3e-90
 Identities = 174/175 (99%)
 Strand = Plus / Plus
```

```
Query: 1317 cattagctttgggaaaagtaatgaaaatataatggttttagaaatcctgtgttaaatatt 1376
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1779 cattagctttgggaaaagtaatgaaaatataatggttttagaaatcctgtgttaaatatt 1838

Query: 1377 gctatattttcttagcagttatttctacagttaattacatagtcatgattgttctacgtt 1436
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1839 gctatattttcttagcagttatttctacagttaattacatagtcatgattgttctacgtt 1898

Query: 1437 tcatatattatatggtgctttgtatatgcccctaataaaatgaatctaaacattg 1491
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct: 1899 tcatatattatatggtgctttgtatatgccactaataaaatgaatctaaacattg 1953
```

The FCTR7 amino acid has 284 of 285 amino acid residues (99%) identical to, and 284 of 285 amino acid residues (99%) similar to, the 500 amino acid Putative secretory protein precursor [*Homo sapiens*] (GenBank-Acc No.: AF142573) (SEQ ID NO:94) (Table 7F).

Table 7F. BLASTP alignments of FCTR7 against Putative secretory protein precursor, (SEQ ID NO:94)

```
>gi|12002311|gb|AAG43287.1|AF142573_1 (AF142573) putative secretory protein
precursor [Homo sapiens]
          Length = 500

 Score =  581 bits (1499), Expect = e-165
 Identities = 284/285 (99%), Positives = 284/285 (99%)

Query: 1   MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDN 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1   MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDN 60

Query: 61  DMQSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESRAESCLWEHGPASLLPSIGQNL 120
           |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct: 61  DMQSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNL 120

Query: 121 GAHWGRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121 GAHWGRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIG 180

Query: 181 CAINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENLC 240
```

```
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  CAINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENLC 240

Query: 241  YKEGSDRYYPPREEETNEIERQQSQVHDTHVRTRSDDSSRNEVIS 285
             |||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  YKEGSDRYYPPREEETNEIERQQSQVHDTHVRTRSDDSSRNEVIS 285
```

The FCTR7 amino acid has 137 of 176 amino acid residues (78%) identical to, and 151 of 176 amino acid residues (86%) similar to, the 188 amino acid Late gestation lung protein 1 [*Rattus norvegicus*] (GenBank-Acc No.: AF109674) (SEQ ID NO:95) (Table 7G).

Table 7G. BLASTP alignments of FCTR7 against Late gestation lung protein 1, (SEQ ID NO:95)

```
>gi|4324682|gb|AAD16986.1| (AF109674) late gestation lung protein 1 [Rattus
norvegicus]
          Length = 188

 Score =  277 bits (709), Expect = 1e-73
 Identities = 137/176 (78%), Positives = 151/176 (86%)

Query: 68   LHNKLRSQVYPTASNMEYMTWDVELERSAESRAESCLWEHGPASLLPSIGQNLGAHWGRY 127
            |||||| |||| |||||||||| ||||||    |  ||||||||||| ||||||   |||||
Sbjct: 2    LHNKLRGQVYPPASNMEYMTWDEELERSAAAWAQRCLWEHGPASLLVSIGQNLAVHWGRY 61

Query: 128  RPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLCH 187
            | | ||||||||||||++||| |||||+|| |||| +||||||+||||+|+||||++ |
Sbjct: 62   RSPGFHVQSWYDEVKDYTYPYPHECNPWCPERCSGAMCTHYTQMVWATTNKIGCAVHTCR 121

Query: 188  NMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYKE 243
            +|++|| ||  |||||||||||||| | |||||||||| || |+||||| ||||+|
Sbjct: 122  SMSVWGDIWENAVYLVCNYSPKGNWIGEAPYKHGRPCSECPSSYGGGCRNNLCYRE 177
```

The FCTR7 amino acid has 130 of 237 amino acid residues (55%) identical to, and 165 of 237 amino acid residues (70%) similar to, the 258 amino acid R3H domain-containing preproprotein; 25 kDa trypsin inhibitor [*Homo sapiens*] (GenBank-Acc No.: D45027) (SEQ ID NO:96) (Table 7H).

Table 7H. BLASTP alignments of FCTR7 against R3H domain-containing preproprotein, 25 kDa trypsin inhibitor (SEQ ID NO:96)

```
>gi|7705676|ref|NP_056970.1| R3H domain-containing preproprotein; 25 kDa
trypsin inhibitor; R3H
           domain (binds single-stranded nucleic acids) containing
           [Homo sapiens]
 gi|2943716|dbj|BAA25066.1| (D45027) 25 kDa trypsin inhibitor [Homo sapiens]
          Length = 258

 Score =  265 bits (678), Expect = 4e-70
 Identities = 130/237 (55%), Positives = 165/237 (70%), Gaps = 3/237 (1%)

Query: 12   TTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDMQSILDLHNK 71
            +||+ +     +     | | +|  |+  +|        | | | || |+ ||| +||| ||+
Sbjct: 20   STVVLLNSTDSSPPTNNFTDIEAALKAQLDSAD---IPKARRKRYISQNDMIAILDYHNQ 76
```

```
Query: 72  LRSQVYPTASNMEYMTWDVELERSAESRAESCLWEHGPASLLPSIGQNLGAHWGRYRPPT 131
           +| +|+| |+||||| ||  |  |||  |   |+|+|||+ ||  +||||    ||||
Sbjct: 77  VRGKVFPPAANMEYMVWDENLAKSAEAWAATCIWDHGPSYLLRFLGQNLSVRTGRYRSIL 136

Query: 132 FHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLCHNMNI 191
             |+ ||||||+++||  +||| || || ||+|||||+|||||||||||+ | |||+
Sbjct: 137 QLVKPWYDEVKDYAFPYPQDCNPRCPMRCFGPMCTHYTQMVWATSNRIGCAIHTCQNMNV 196

Query: 192 WGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYKEGSDRY 248
           || +| +|||||||+||||| | |||| | |||+||||+|| | +|||+   +  |
Sbjct: 197 WGSVWRRAVYLVCNYAPKGNWIGEAPYKVGVPCSSCPPSYGGSCTDNLCFPGVTSNY 253
```

The FCTR7 amino acid has 109 of 233 amino acid residues (47%) identical to, and 146 of 233 amino acid residues (63%) similar to, the 253 amino acid Novel protein similar to a trypsin inhibitor [*Homo sapiens*] 25 kDa trypsin inhibitor (EMBLAcc No.: AL117382) (SEQ ID NO:97) (Table 7I).

Table 7I. BLASTP alignments of FCTR7 against Novel protein similar to a trypsin inhibitor, (SEQ ID NO:97)

```
>gi|9885193|emb|CAC04190.1| (AL117382) dJ881L22.3 (novel protein similar to a
trypsin
          inhibitor) [Homo sapiens]
         Length = 253

 Score =  225 bits (575), Expect = 4e-58
 Identities = 109/233 (47%), Positives = 146/233 (63%), Gaps = 8/233 (3%)

Query: 10  RVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDMQSILDLH 69
           +    | |  | ||   | +| +  |          + + | || |+  || ++|| |
Sbjct: 19  QAVNALIMPNATPAPAQPESTAMRLL--------SGLEVPRYRRKRHISVRDMNALLDYH 70

Query: 70  NKLRSQVYPTASNMEYMTWDVELERSAESRAESCLWEHGPASLLPSIGQNLGAHWGRYRP 129
           | +|+ ||| |+||||| ||  | | ||  |  |+| |||+ |+  +||||  | |+||
Sbjct: 71  NHIRASVYPPAANMEYMVWDKRLARAAEAWATQCIWAHGPSQLMRYVGQNLSIHSGQYRS 130

Query: 130 PTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLCHNM 189
               ++|| +|   + +|   +|||+||+|| || |+||||+|||+|||+||||+ | ++
Sbjct: 131 VVDLMKSWSEEKWHYLFPAPRDCNPHCPWRCDGPTCSHYTQMVWASSNRLGCAIHTCSSI 190

Query: 190 NIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYK 242
           ++||  | +| ||||||+ |||| | +||| |+|||+|||||+ | |  |+|+|
Sbjct: 191 SVWGNTWHRAAYLVCNYAIKGNWIGESPYKMGKPCSSCPPSYQGSCNSNMCFK 243
```

The FCTR7 amino acid has 129 of 237 amino acid residues (54%) identical to, and 167 of 237 amino acid residues (70%) similar to, the 258 amino acid 25 kDa Trypsin Inhibitor from *Homo sapiens* (EMBLAcc No.: O43692) (SEQ ID NO:88) (Table 7J).

Table 7J. BLASTP alignments of FCTR7 against 25 kDa Trypsin Inhibitor, (SEQ ID NO:88)

```
ptnr:SPTREMBL-ACC:O43692 25 KDA TRYPSIN INHIBITOR - Homo sapiens (Human), 258
aa.
Score = 743 (261.5 bits), Expect = 1.6e-73, P = 1.6e-73
 Identities = 129/237 (54%), Positives = 167/237 (70%)
```

The FCTR7 amino acid has 79 of 193 amino acid residues (40%) identical to, and 110 of 193 amino acid residues (56%) similar to, the 266 amino acid Glioma Pathogenesis-Related Protein (RTVP-1 Protein) - *Homo sapiens* (SWISSPROT Acc No.: P48060) (SEQ ID NO:90) (Table 7K).

Table 7K. BLASTP alignments of FCTR7 against Glioma Pathogenesis-Related Protein, (SEQ ID NO:90)

```
ptnr:SWISSPROT-ACC:P48060 GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN)
- Homo sapiens (Human), 266 aa
Score = 314 (110.5 bits), Expect = 4.7e-28, P = 4.7e-28
 Identities = 79/193 (40%), Positives = 110/193 (56%)
```

The FCTR7 amino acid has 66 of 186 amino acid residues (35%) identical to, and 91 of 186 amino acid residues (48%) similar to, the 186 amino acid Neutrophil granules matrix glycoprotein SGP28 precursor from *Homo sapiens* (SWISSPROT Acc No.: S68691) (SEQ ID NO:98) (Table 7L).

Table 7L. BLASTP alignments of FCTR7 against Neutrophil granules matrix glycoprotein, (SEQ ID NO:98)

```
ptnr:PIR-ID:S68691 neutrophil granules matrix glycoprotein SGP28 precursor -
human
Score = 254 (89.4 bits), Expect = 1.1e-21, P = 1.1e-21
 Identities = 66/186 (35%), Positives = 91/186 (48%)
```

A novel developmentally regulated gene with homology to a tumor derived trypsin inhibitor is expressed in lung mesenchyme, as described in Am. J. Physiol. 0:0-0(1999). cDNA cloning of a novel trypsin inhibitor with similarity to pathogenesis-related proteins, and its frequent expression in human brain cancer cells is disclosed in Biochim. Biophys. Acta 1395:202-208(1998). RTVP-1, a novel human gene with sequence similarity to genes of diverse species, is expressed in tumor cell lines of glial but not neuronal origin, as published in Gene 180:125-130(1996). The human glioma pathogenesis-related protein is structurally related to plan pathogenesis-related proteins and its gene is expressed specifically in brain tumors (Gene 159:131-135(1995)). Structure comparison of human glioma pathogenesis-related protein GliPR and the plant pathogenesis-related protein P14a indicates a functional link between the human

immune system and a plant defense system (Proc. Natl. Acad. Sci. U.S.A. 95:2262-2266(1998)). GliPR is highly expressed in the human brain tumor, glioblastoma multiform/astrocytome, but neither in normal fetal or adult brain tissue, nor in other nervous system tumors. GliPR belongs to a family that groups mammalian SCP/TPX1; insects AG3/AG5; FUNGI SC7/SC14 and plants PR-1. SGP28, a novel matrix glycoprotein in specific granules of human neutrophils with similarity to a human testis-specific gene product and to a rodent sperm-coating glycoprotein (FEBS Lett. 380, 246-250, 1996). The primary structure and properties of helothermine, a peptide toxin that blocks ryanodine receptors is described in Biophys. J. 68:2280-2288(1995). As GliPR, Helothermine belongs to a family that groups mammalian SCP/TPX1; insects AG3/AG5; FUNGI SC7/SC14 and plants PR-1.

Based upon homology, FCTR7 protein and each homologous protein or peptide may share at least some activity.

Therapeutic uses:

FCTR7 protein has homology to trypsin inhibitors, Q91055 helothermine, tumor derived tyrpsin inhibitors, glioma pathogenesis-related protein, `Q9Z0U6 LATE GESTATION LUNG PROTEIN 1,` and to the Prosite family which groups mammalian SCP/TPX1;INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1 proteins. Therefore the FCTR7 protein disclosed in this invention could function like the proteins which it has homology to. These functions include tissue development *in vitro* and *in vivo*, and cancer pathogenesis.

Based the tissue expression pattern, the gene is implicated in diseases of tissues in which it is expressed. These diseases include but are not limited to:

- Glioma,
- cancer,
- lung diseases,
- gestation,
- male and female reproductive diseases,
- deafness,
- neurological disorders,
- gastric disorders, and
- pancreatic diseases like diabetes.

These materials are further useful in the generation of antibodies that bind immunospecifically to the novel FCTR7 substances for use in therapeutic or diagnostic methods.

These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-FCTRX Antibodies" section below. In one embodiment, a contemplated FCTR7 epitope is from aa 40 to 120. In another embodiment, a FCTR7 epitope is from aa 130 to 170. In additional embodiments, FCTR7 epitopes are from aa 210 to 230, and from aa 240 to 280.

TABLE 8A: Summary Of Nucleic Acids And Proteins Of The Invention

Name	Tables	Clone; Description of Homolog	Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO
FCTR1	1A, 1B,	58092213.0.36 follistatin-like protein	1	2
FCTR2	2A, 2B	AC012614_1.0.123; KIAA1061-like protein	3	4
FCTR3	3A, 3B	10129612.0.118; neurestin-like protein	5	6
	3C, 3D	10129612.0.405; neurestin-like protein	7	8
	3E	10129612.0.154; neurestin-like protein	9	
	3F	10129612.0.67; neurestin-like protein	10	
	3G	10129612.0.258; neurestin-like protein	11	
	3H, 3I	10129612.0.352; neurestin-like protein	12	13
FCTR4	4A, 4B	29692275.0.1; NF-Kappa-B P65delta3-like protein	14	15
FCTR5	5A, 5B	32125243.0.21; human complement C1R component precursor -like protein	16	17
	5C, 5D		18	19
FCTR6	6A, 6B	27455183.0.19; novel human blood coagulation factor XI -like protein	20	21
	6C, 6D	27455183.0.145; novel human blood coagulation factor XI -like protein	22	23
FCTR7	7A, 7B	32592466.0.64; trypsin inhibitor -like protein	24	25
FCTR1	Example 2	Ag809 Forward	26	
FCTR1	Example 2	Ag809 Probe	27	
FCTR1	Example 2	Ag809 Reverse	28	
FCTR4	Example 2	Ag2773 Forward	29	
FCTR4	Example 2	Ag2773 Probe	30	
FCTR4	Example 2	Ag2773 Reverse	31	
FCTR5	Example 2	Ag427 Forward	32	
FCTR5	Example 2	Ag427 Probe	33	
FCTR5	Example 2	Ag427 Reverse	34	
FCTR6	Example 2	Ag1541 Forward	35	
FCTR6	Example 2	Ag1541 Probe	36	
FCTR6	Example 2	Ag1541 Reverse	37	

TABLE 8B: Summary of Query Sequences Disclosed

Table	Database	Acc. No.	Sequence Name	Species	SEQ ID NO.
1C, 1K	remtrEmbl	BAA21725	IGFBP-like protein	mouse	38
1D	sptrEmbl	Q61581	Follistatin-like protein-2	Mouse	39

1E	SptrEmbl	Q07822	Mac25 protein	Human	40
1F, 1K	SptrEmbl	O88812	Mac25 protein	Mouse	41
1G, 1K	SptrEmbl	Q16270	Prostacyclin-stimulating factor	Human	42
1H, 1K	PIR	B40098	Colorectal cancer suppressor	Rat	43
1I	TrEmblnew	AAD9360	PTP sigma (brain) precursor	Human	44
1J	SptrEmbl	Q13332	PTP sigma precursor	Human	45
2C	GenBank	AB028984	KIAA1061 cDNA	Human	46
2D	TrEmblnew	BAA85677	KIAA1263	Human	47
2E	TrEmblnew	BAA83013	KIAA1061 protein fragment	Human	48
2F	Embl	CAB70877.1	Hypothetical protein DKFzp566D234.1	Human	49
2G	GenBank	Q62632	Follistatin-related protein-1 precursor	Rat	50
2H	GenBank	Q62536	Follistatin-related protein-1 precursor	Mouse	51
2I	GenBank	JG0187	Follistatin related protein	African clawed frog	52
2J	GenBank	Q12841	Follistatin related protein-1 precursor	Human	53
2K	Embl	CAB42968.1	Flik protein	Chicken	54
2L	GenBank	T13822	Frazzled gene protein	Fruit fly	55
2M	GenBank	AAC38849.1	Roundabout 1	Fruit fly	56
2N	GenBank	O60469	Down Syndrome Cell Adhesion Molecule Precursor	Human`	57
2O	SwissProt	Q13449	Limbic system-associated membrane protein precursor	Human	58
2P	SptrEmbl	O70246	Putative neuronal cell adhesion molecule, short form	Mouse	59
2Q	SptrEmbl	O02869	CHLAMP, G11-isoform precursor	Chicken	60
2R	SwissProt	Q62813	Limbic system-associated membrane protein precursor	Rat	61
3J	GenBank	NM_011856.2	Odd Oz/ten-m homology 2	Fruit fly	62
3K	Embl	AJ245711.1	Teneurin-2 cDNA, short splice variant	Chicken	63
3L	GenBank	AB032953	KIAA 1127 cDNA	Human	64
3M, 3U	GenBank	AB025411	Ten-m2 cDNA	Mouse	65
3N	GenBank	NM_020088.1	Neurestin alpha cDNA	Rat	66
3O	Embl	GGA278031	Teneurin-2	Chicken	67
3P	GenBank	NP_035986.2	Odd Oz/ten-m homology 2	Fruit fly	68
3Q	Embl	CAC09416.1	Teneurin-2	Chicken	69
3R	GenBank	BAA77399.1	Ten-m4	Mouse	70
3S	GenBank	AB032953	KIAA1127 protein	Human	71
3T	GenBank	AF086607	Neurestin alpha	Rat	72
4C	SptrEmbl	Q99233	Hypothetical 10 kD protein	Trypanosome	73
4C	SptrEmbl	Q16896	GABA receptor subunit		74
4C	SptrEmbl	O76473	GABA receptor subunit		75
4C	TrEmblnew	AAD28317	FI3J11.13 protein		76

Text p. 90	SptrEmbl	Q13313	NF-kappa B P65 delta 3 protein	Human	77
5E	GenBank	XM_007061.1	Complement C1R-like proteinase precursor	Human	78
5F	GenBank	NM_001733.1	Complement component 1, R subcomponent cDNA	Human	79
5G	GenBank	AAF44349.1	Complement C1R-like proteinase precursor	Human	80
5H	GenBank	AAA5185.1	Complement C1R component precursor	Human	81
6E	GenBank	AB046651	Brain cDNA clone Qcc-17034	Macaque	82
6F	GenBank	AK09660	Adult testis cDNA, RIKEN full length enriched	Mouse	83
6G	GenBank	AB046651	Hypothetical protein	Macaque	84
6H	GenBank	NP_000838.1	Plasma kallikrein B1 precursor	Human	85
6I	GenBank	BAA37147.1	Kallikrein	Pig	86
6J	Embl	CAA64368.1	Coagulation factor XI	Human	87
7D, 7J	SptrEmbl	O43692	25 kDa trypsin inhibitor	Human	88
7D	SptrEmbl	O44228	HRTT-1		89
7D, 7K	SptrEmbl	P418060	Glioma pathogenesis-related protein	Human	90
7D	PIR-ID	JC4131	Glioma pathogenesis-related protein	Human	91
7D	SwissProt	O19010	Cysteine-rcih secretory protein		92
7E	GenBank	AF142573	Putatitive secretory protein precursor cDNA	Human	93
7F	GenBank	AF142573	Putative secretory protein precursor	Human	94
7G	GenBank	AF109674	Late gestation lung protein 1	Rat	95
7H	GenBank	D45027	R3H domain containing preprotein, 25 kDa trypsin inhibitor	Human	96
7I	Embl	AL117382	Novel protein similar to a trypsin inhibitor	Human	97
7L	PIR-ID	S68691	Neutrophil granules matrix glycoprotein SGP28 precursor	Human	98

FCTRX Nucleic Acids and Polypeptides

One aspect of the invention pertains to isolated nucleic acid molecules that encode FCTRX polypeptides or biologically-active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify FCTRX-encoding nucleic acids (*e.g.*, FCTRX mRNAs) and fragments for use as PCR primers for the amplification and/or mutation of FCTRX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule may be single-stranded or double-stranded, but preferably is comprised double-stranded DNA.

An FCTRX nucleic acid can encode a mature FCTRX polypeptide. As used herein, a "mature" form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an ORF described herein. The product "mature" form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a "mature" form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an ORF, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

The term "probes", as utilized herein, refers to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as approximately, *e.g.*, 6,000 nt, depending upon the specific use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are generally obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

The term "isolated" nucleic acid molecule, as utilized herein, is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated FCTRX nucleic acid molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb,

0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, etc.). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, or a complement of this aforementioned nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24 as a hybridization probe, FCTRX molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, *et al.*, (eds.), MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to FCTRX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, or a portion of this nucleotide sequence (*e.g.*, a

fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an FCTRX polypeptide). A nucleic acid molecule that is complementary to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, is one that is sufficiently complementary to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, thereby forming a stable duplex.

As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or

when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below.

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of FCTRX polypeptides. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the invention, homologous nucleotide sequences include nucleotide sequences encoding for an FCTRX polypeptide of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the exact nucleotide sequence encoding human FCTRX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, as well as a polypeptide possessing FCTRX biological activity. Various biological activities of the FCTRX proteins are described below.

An FCTRX polypeptide is encoded by the open reading frame ("ORF") of an FCTRX nucleic acid. An ORF corresponds to a nucleotide sequence that could potentially be translated into a polypeptide. A stretch of nucleic acids comprising an ORF is uninterrupted by a stop codon. An ORF that represents the coding sequence for a full protein begins with an ATG "start" codon and terminates with one of the three "stop" codons, namely, TAA, TAG, or TGA. For the purposes of this invention, an ORF may be any part of a coding sequence, with or without a start codon, a stop codon, or both. For an ORF to be considered as a good candidate for coding for a *bona fide* cellular protein, a minimum size requirement is often set, *e.g.*, a stretch of DNA that would encode a protein of 50 amino acids or more.

The nucleotide sequences determined from the cloning of the human FCTRX genes allows for the generation of probes and primers designed for use in identifying and/or cloning FCTRX homologues in other cell types, *e.g.* from other tissues, as well as FCTRX homologues from other vertebrates. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that

hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24; or an anti-sense strand nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24; or of a naturally occurring mutant of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24.

Probes based on the human FCTRX nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues which mis-express an FCTRX protein, such as by measuring a level of an FCTRX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting FCTRX mRNA levels or determining whether a genomic FCTRX gene has been mutated or deleted.

"A polypeptide having a biologically-active portion of an FCTRX polypeptide" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically-active portion of FCTRX" can be prepared by isolating a portion of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, that encodes a polypeptide having an FCTRX biological activity (the biological activities of the FCTRX proteins are described below), expressing the encoded portion of FCTRX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of FCTRX.

FCTRX Nucleic Acid and Polypeptide Variants

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, due to degeneracy of the genetic code and thus encode the same FCTRX proteins as that encoded by the nucleotide sequences shown in SEQ ID NO NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25.

In addition to the human FCTRX nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the FCTRX

polypeptides may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the FCTRX genes may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an FCTRX protein, preferably a vertebrate FCTRX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the FCTRX genes. Any and all such nucleotide variations and resulting amino acid polymorphisms in the FCTRX polypeptides, which are the result of natural allelic variation and that do not alter the functional activity of the FCTRX polypeptides, are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding FCTRX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the FCTRX cDNAs of the invention can be isolated based on their homology to the human FCTRX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500, 750, 1000, 1500, or 2000 or more nucleotides in length. In yet another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.,* nucleic acids encoding FCTRX proteins derived from species other than human) or other related sequences (*e.g.,* paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase “stringent hybridization conditions” refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal

melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at Tm, 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions are hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C, followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequences of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well-known within the art. See, *e.g.*, Ausubel, et *al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990; GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequences of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*, Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981. *Proc Natl Acad Sci USA* **78**: 6789-6792.

Conservative Mutations

In addition to naturally-occurring allelic variants of FCTRX sequences that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences of SEQ ID NO NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, thereby leading to changes in the amino acid sequences of the encoded FCTRX proteins, without altering the functional ability of said FCTRX proteins. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the FCTRX proteins without altering their biological activity, whereas an "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the FCTRX proteins of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known within the art.

Another aspect of the invention pertains to nucleic acid molecules encoding FCTRX proteins that contain changes in amino acid residues that are not essential for activity. Such FCTRX proteins differ in amino acid sequence from SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45% homologous to the amino acid sequences of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25. Preferably, the protein encoded by the nucleic acid molecule is at least about 60% homologous to SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25; more

preferably at least about 70% homologous to SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25; still more preferably at least about 80% homologous to SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25; even more preferably at least about 90% homologous to SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25; and most preferably at least about 95% homologous to SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25.

An isolated nucleic acid molecule encoding an FCTRX protein homologous to the protein of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted, non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined within the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted non-essential amino acid residue in the FCTRX protein is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an FCTRX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for FCTRX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

The relatedness of amino acid families may also be determined based on side chain interactions. Substituted amino acids may be fully conserved “strong” residues or fully conserved “weak” residues. The “strong” group of conserved amino acid residues may be any one of the following groups: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW, wherein the single letter amino acid codes are grouped by those amino acids that may be substituted for each other. Likewise, the “weak” group of conserved residues may be any one of

the following: CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK, NEQHRK, VLIM, HFY, wherein the letters within each group represent the single letter amino acid code.

In one embodiment, a mutant FCTRX protein can be assayed for (*i*) the ability to form protein:protein interactions with other FCTRX proteins, other cell-surface proteins, or biologically-active portions thereof, (*ii*) complex formation between a mutant FCTRX protein and an FCTRX ligand; or (*iii*) the ability of a mutant FCTRX protein to bind to an intracellular target protein or biologically-active portion thereof; (*e.g.* avidin proteins).

In yet another embodiment, a mutant FCTRX protein can be assayed for the ability to regulate a specific biological function (*e.g.*, regulation of insulin release).

Antisense Nucleic Acids

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein (*e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence). In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire FCTRX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of an FCTRX protein of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25; or antisense nucleic acids complementary to an FCTRX nucleic acid sequence of SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24, are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an FCTRX protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding the FCTRX protein. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding the FCTRX protein disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and

Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of FCTRX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of FCTRX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of FCTRX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally-occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids (*e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used).

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an FCTRX protein to thereby inhibit expression of the protein (*e.g.*, by inhibiting transcription and/or translation). The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the

double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface (*e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens). The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient nucleic acid molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other. See, *e.g.*, Gaultier, *et al.*, 1987. *Nucl. Acids Res.* **15**: 6625-6641. The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (see, *e.g.*, Inoue, *et al.* 1987. *Nucl. Acids Res.* **15**: 6131-6148) or a chimeric RNA-DNA analogue (see, *e.g.*, Inoue, *et al.*, 1987. *FEBS Lett.* **215**: 327-330.

Ribozymes and PNA Moieties

Nucleic acid modifications include, by way of non-limiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In one embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes as described in Haselhoff and Gerlach 1988. *Nature* 334: 585-591) can be used to catalytically cleave FCTRX mRNA transcripts to thereby inhibit translation of FCTRX mRNA. A ribozyme having specificity for an FCTRX-encoding nucleic acid can be designed based upon the nucleotide sequence of an FCTRX cDNA disclosed herein (*i.e.*, SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an FCTRX-encoding mRNA. See, *e.g.*, U.S. Patent 4,987,071 to Cech, *et al.* and U.S. Patent

5,116,742 to Cech, *et al*. FCTRX mRNA can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al*., (1993) *Science* 261:1411-1418.

Alternatively, FCTRX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the FCTRX nucleic acid (*e.g.*, the FCTRX promoter and/or enhancers) to form triple helical structures that prevent transcription of the FCTRX gene in target cells. *See, e.g.,* Helene, 1991. *Anticancer Drug Des.* 6: 569-84; Helene, *et al.* 1992. *Ann. N.Y. Acad. Sci.* 660: 27-36; Maher, 1992. *Bioassays* 14: 807-15.

In various embodiments, the FCTRX nucleic acids can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids. *See, e.g.,* Hyrup, *et al*., 1996. *Bioorg Med Chem* 4: 5-23. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (*e.g.*, DNA mimics) in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup, *et al*., 1996. *supra*; Perry-O'Keefe, *et al*., 1996. *Proc. Natl. Acad. Sci. USA* 93: 14670-14675.

PNAs of FCTRX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of FCTRX can also be used, for example, in the analysis of single base pair mutations in a gene (*e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S_1 nucleases (*see,* Hyrup, *et al.,* 1996.*supra*); or as probes or primers for DNA sequence and hybridization (*see,* Hyrup, *et al*., 1996, *supra*; Perry-O'Keefe, *et al.,* 1996. *supra*).

In another embodiment, PNAs of FCTRX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of FCTRX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (*e.g.*, RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using

linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (*see,* Hyrup, etal., 1996. *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, *et al.,* 1996. *supra* and Finn, *et al*., 1996. *Nucl Acids Res* 24: 3357-3363. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA. *See, e.g.,* Mag, *et al*., 1989. *Nucl Acid Res* 17: 5973-5988. PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment. *See, e.g.,* Finn, *et al*., 1996. *supra.* Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. *See, e.g.,* Petersen, *et al*., 1975. *Bioorg. Med. Chem. Lett.* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g*., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (*see, e.g*., Letsinger, *et al*., 1989. *Proc. Natl. Acad. Sci. U.S.A.* 86: 6553-6556; Lemaitre, *et al*., 1987. *Proc. Natl. Acad. Sci.* 84: 648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (*see, e.g*., PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (*see, e.g.,* Krol, *et al*., 1988. *BioTechniques* 6:958-976) or intercalating agents (*see, e.g*., Zon, 1988. *Pharm. Res*. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g*., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

FCTRX Polypeptides

A polypeptide according to the invention includes a polypeptide including the amino acid sequence of FCTRX polypeptides whose sequences are provided in SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, while still encoding a protein that maintains its FCTRX activities and physiological functions, or a functional fragment thereof.

In general, an FCTRX variant that preserves FCTRX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the

invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

One aspect of the invention pertains to isolated FCTRX proteins, and biologically-active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-FCTRX antibodies. In one embodiment, native FCTRX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, FCTRX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, an FCTRX protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" polypeptide or protein or biologically-active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the FCTRX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of FCTRX proteins in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly-produced. In one embodiment, the language "substantially free of cellular material" includes preparations of FCTRX proteins having less than about 30% (by dry weight) of non-FCTRX proteins (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-FCTRX proteins, still more preferably less than about 10% of non-FCTRX proteins, and most preferably less than about 5% of non-FCTRX proteins. When the FCTRX protein or biologically-active portion thereof is recombinantly-produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the FCTRX protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of FCTRX proteins in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of FCTRX proteins having less than about 30% (by dry weight) of chemical precursors or non-FCTRX chemicals, more preferably less than about 20% chemical precursors or non-FCTRX chemicals, still more preferably less than about 10% chemical precursors or non-FCTRX chemicals, and most preferably less than about 5% chemical precursors or non-FCTRX chemicals.

Biologically-active portions of FCTRX proteins include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of the FCTRX proteins (*e.g.*, the amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25) that include fewer amino acids than the full-length FCTRX proteins, and exhibit at least one activity of an FCTRX protein. Typically, biologically-active portions comprise a domain or motif with at least one activity of the FCTRX protein. A biologically-active portion of an FCTRX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acid residues in length.

Moreover, other biologically-active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native FCTRX protein.

In an embodiment, the FCTRX protein has an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25. In other embodiments, the FCTRX protein is substantially homologous to SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, and retains the functional activity of the protein of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail, below. Accordingly, in another embodiment, the FCTRX protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino acid sequence of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, and retains the functional activity of the FCTRX proteins of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25.

Determining Homology Between Two or More Sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. *See,* Needleman and Wunsch, 1970. *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty

of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 10, 11, 12, 14, 16, 18, 20, 22, and 24.

The term “sequence identity” refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term “percentage of sequence identity” is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.,* A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.,* the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term “substantial identity” as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region.

Chimeric and Fusion Proteins

The invention also provides FCTRX chimeric or fusion proteins. As used herein, an FCTRX "chimeric protein" or "fusion protein" comprises an FCTRX polypeptide operatively-linked to a non-FCTRX polypeptide. An "FCTRX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an FCTRX protein (SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25), whereas a "non-FCTRX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the FCTRX protein, *e.g.*, a protein that is different from the FCTRX protein and that is derived from the same or a different organism. Within an FCTRX fusion protein the FCTRX polypeptide can correspond to all or a portion of an FCTRX protein. In one embodiment, an FCTRX fusion protein comprises at least one biologically-active portion of an FCTRX protein. In another embodiment, an FCTRX fusion protein comprises at least two biologically-active portions of an FCTRX protein. In yet another embodiment, an FCTRX fusion protein comprises at least three biologically-active portions of an FCTRX protein. Within the fusion protein, the term "operatively-linked" is intended to indicate that the FCTRX polypeptide and the non-FCTRX polypeptide are fused in-frame with one another. The non-FCTRX polypeptide can be fused to the N-terminus or C-terminus of the FCTRX polypeptide.

In one embodiment, the fusion protein is a GST-FCTRX fusion protein in which the FCTRX sequences are fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant FCTRX polypeptides.

In another embodiment, the fusion protein is an FCTRX protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of FCTRX can be increased through use of a heterologous signal sequence.

In yet another embodiment, the fusion protein is an FCTRX-immunoglobulin fusion protein in which the FCTRX sequences are fused to sequences derived from a member of the immunoglobulin protein family. The FCTRX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between an FCTRX ligand and an FCTRX protein on the surface of a cell, to thereby suppress FCTRX-mediated signal transduction *in vivo*. The FCTRX-immunoglobulin fusion proteins can be used to affect the bioavailability of an FCTRX cognate ligand. Inhibition of the FCTRX ligand/FCTRX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the FCTRX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-FCTRX antibodies in a subject, to purify FCTRX ligands, and in screening assays to identify molecules that inhibit the interaction of FCTRX with an FCTRX ligand.

An FCTRX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (*see, e.g.,* Ausubel, *et al.* (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An FCTRX-encoding nucleic acid

can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the FCTRX protein.

FCTRX Agonists and Antagonists

The invention also pertains to variants of the FCTRX proteins that function as either FCTRX agonists (*i.e.,* mimetics) or as FCTRX antagonists. Variants of the FCTRX protein can be generated by mutagenesis (*e.g.*, discrete point mutation or truncation of the FCTRX protein). An agonist of the FCTRX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the FCTRX protein. An antagonist of the FCTRX protein can inhibit one or more of the activities of the naturally occurring form of the FCTRX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the FCTRX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the FCTRX proteins.

Variants of the FCTRX proteins that function as either FCTRX agonists (*i.e.,* mimetics) or as FCTRX antagonists can be identified by screening combinatorial libraries of mutants (*e.g.*, truncation mutants) of the FCTRX proteins for FCTRX protein agonist or antagonist activity. In one embodiment, a variegated library of FCTRX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of FCTRX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential FCTRX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of FCTRX sequences therein. There are a variety of methods which can be used to produce libraries of potential FCTRX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential FCTRX sequences. Methods for synthesizing degenerate oligonucleotides are well-known within the art. *See, e.g.,* Narang, 1983. *Tetrahedron* 39: 3; Itakura, *et al.*, 1984. *Annu. Rev. Biochem.* 53: 323; Itakura, *et al.*, 1984. *Science* 198: 1056; Ike, *et al.*, 1983. *Nucl. Acids Res.* 11: 477.

Polypeptide Libraries

In addition, libraries of fragments of the FCTRX protein coding sequences can be used to generate a variegated population of FCTRX fragments for screening and subsequent selection of variants of an FCTRX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an FCTRX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double-stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S_1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, expression libraries can be derived which encodes N-terminal and internal fragments of various sizes of the FCTRX proteins.

Various techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of FCTRX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify FCTRX variants. *See, e.g.,* Arkin and Yourvan, 1992. *Proc. Natl. Acad. Sci. USA* 89: 7811-7815; Delgrave, *et al.*, 1993. *Protein Engineering* 6:327-331.

Anti-FCTRX Antibodies

The invention encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the FCTRX polypeptides of said invention.

An isolated FCTRX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind to FCTRX polypeptides using standard techniques for polyclonal and monoclonal antibody preparation. The full-length FCTRX proteins can be used or, alternatively, the invention provides antigenic peptide fragments of FCTRX proteins for use as immunogens. The antigenic FCTRX peptides comprises at least 4 amino acid residues of the amino acid sequence shown in SEQ ID NO NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, and

encompasses an epitope of FCTRX such that an antibody raised against the peptide forms a specific immune complex with FCTRX. Preferably, the antigenic peptide comprises at least 6, 8, 10, 15, 20, or 30 amino acid residues. Longer antigenic peptides are sometimes preferable over shorter antigenic peptides, depending on use and according to methods well known to someone skilled in the art.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of FCTRX that is located on the surface of the protein (*e.g.*, a hydrophilic region). As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation (*see, e.g.*, Hopp and Woods, 1981. *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle, 1982. *J. Mol. Biol.* 157: 105-142, each incorporated herein by reference in their entirety).

As disclosed herein, FCTRX protein sequences of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically-active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically-binds (immunoreacts with) an antigen, such as FCTRX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human FCTRX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to an FCTRX protein sequence of SEQ ID NOS:2, 4, 6, 8, 13, 15, 17, 19, 21, 23, and 25, or a derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed FCTRX protein or a chemically-synthesized FCTRX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar

immunostimulatory agents. If desired, the antibody molecules directed against FCTRX can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of FCTRX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular FCTRX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular FCTRX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (*see, e.g.*, Kohler & Milstein, 1975. *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (*see, e.g.*, Kozbor, *et al.*, 1983. *Immunol. Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (*see, e.g.*, Cole, *et al.*, 1985. In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the invention and may be produced by using human hybridomas (*see, e.g.*, Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (*see, e.g.*, Cole, *et al.*, 1985. In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations is incorporated herein by reference in their entirety.

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an FCTRX protein (*see, e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (*see, e.g.*, Huse, *et al.*, 1989. *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for an FCTRX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. *See, e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to an FCTRX protein may be produced by techniques known in the art including, but not limited to: (*i*) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (*ii*) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (*iii*) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent; and (*iv*) F_v fragments.

Additionally, recombinant anti-FCTRX antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made

using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Patent No. 4,816,567; U.S. Pat. No. 5,225,539; European Patent Application No. 125,023; Better, *et al.*, 1988. *Science* 240: 1041-1043; Liu, *et al.*, 1987. *Proc. Natl. Acad. Sci. USA* 84: 3439-3443; Liu, *et al.*, 1987. *J. Immunol.* 139: 3521-3526; Sun, *et al.*, 1987. *Proc. Natl. Acad. Sci. USA* 84: 214-218; Nishimura, *et al.*, 1987. *Cancer Res.* 47: 999-1005; Wood, *et al.*, 1985. *Nature* 314 :446-449; Shaw, *et al.*, 1988. *J. Natl. Cancer Inst.* 80: 1553-1559); Morrison(1985) *Science* 229:1202-1207; Oi, *et al.* (1986) *BioTechniques* 4:214; Jones, *et al.*, 1986. *Nature* 321: 552-525; Verhoeyan, *et al.*, 1988. *Science* 239: 1534; and Beidler, *et al.*, 1988. *J. Immunol.* 141: 4053-4060. Each of the above citations are incorporated herein by reference in their entirety.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of an FCTRX protein is facilitated by generation of hybridomas that bind to the fragment of an FCTRX protein possessing such a domain. Thus, antibodies that are specific for a desired domain within an FCTRX protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-FCTRX antibodies may be used in methods known within the art relating to the localization and/or quantitation of an FCTRX protein (*e.g.*, for use in measuring levels of the FCTRX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for FCTRX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds (hereinafter "Therapeutics").

An anti-FCTRX antibody (*e.g.*, monoclonal antibody) can be used to isolate an FCTRX polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-FCTRX antibody can facilitate the purification of natural FCTRX polypeptide from cells and of recombinantly-produced FCTRX polypeptide expressed in host cells. Moreover, an anti-FCTRX antibody can be used to detect FCTRX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the FCTRX protein. Anti-FCTRX antibodies can be used diagnostically to monitor protein levels in tissue as part of a

clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

FCTRX Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an FCTRX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis